

09/701395

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O.G. FIG.	SUBCLASS	
	CLASS	
APPROVED BY	DRAFTSMAN	

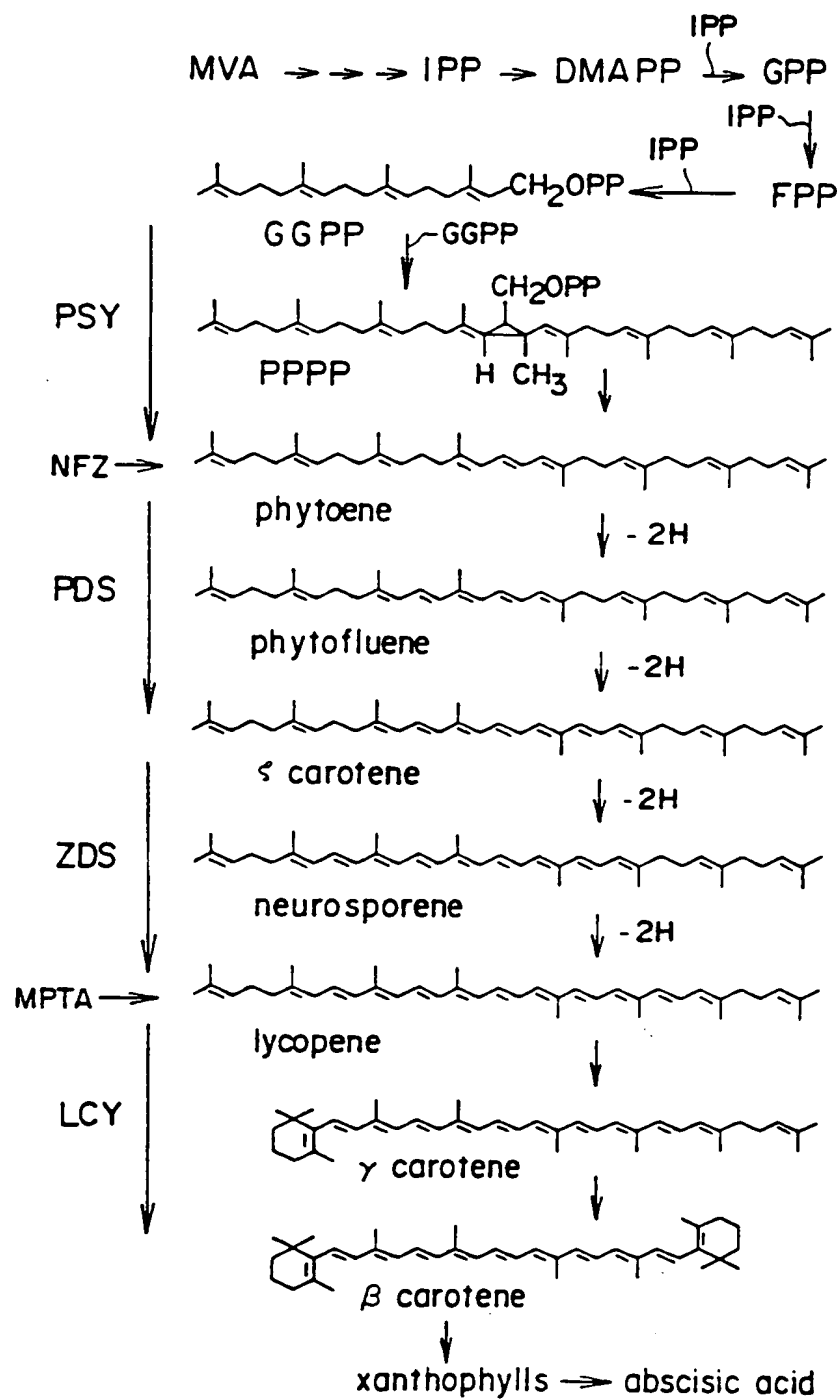


FIG. 1

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	DRAGTSMAN		

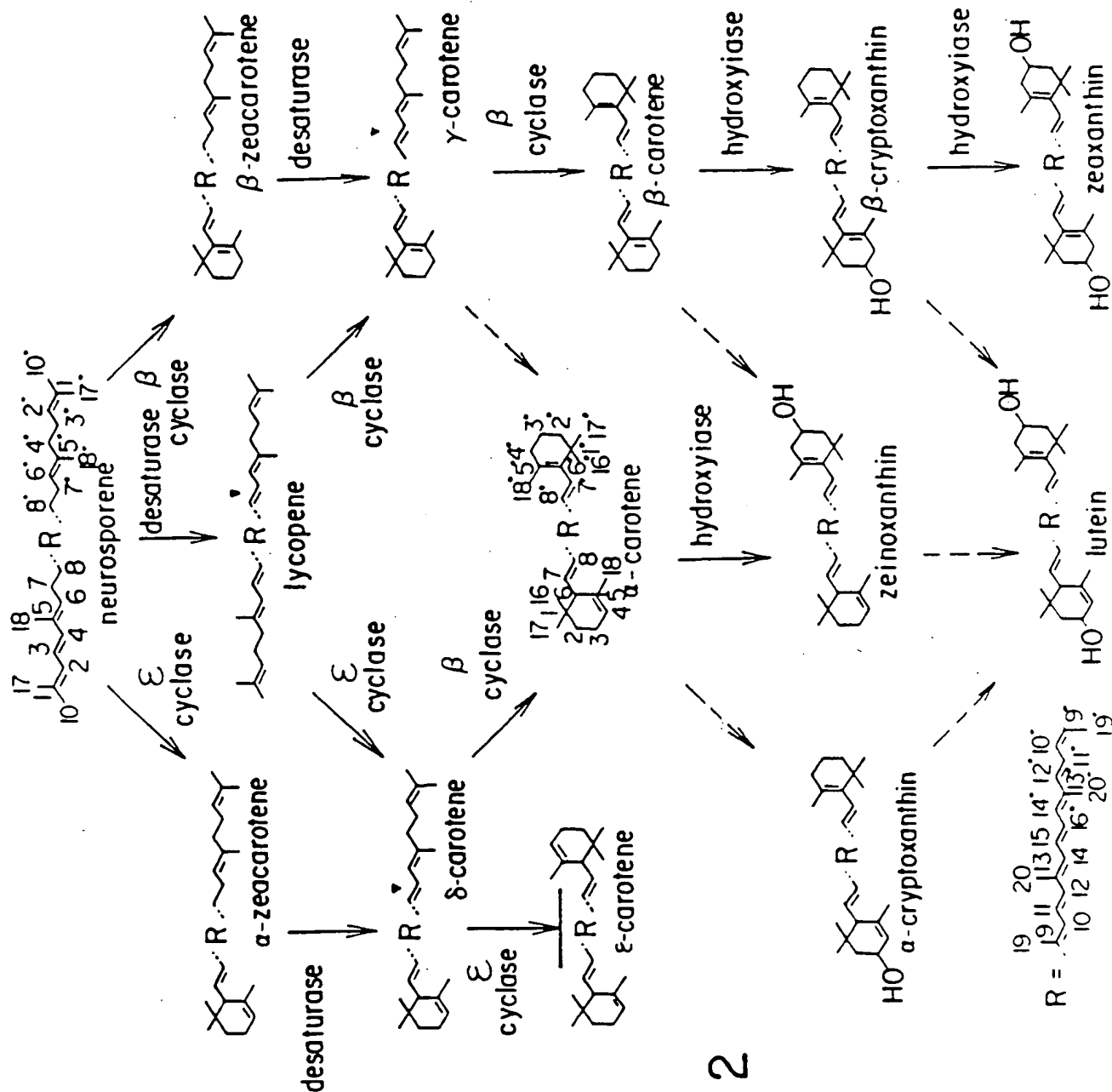
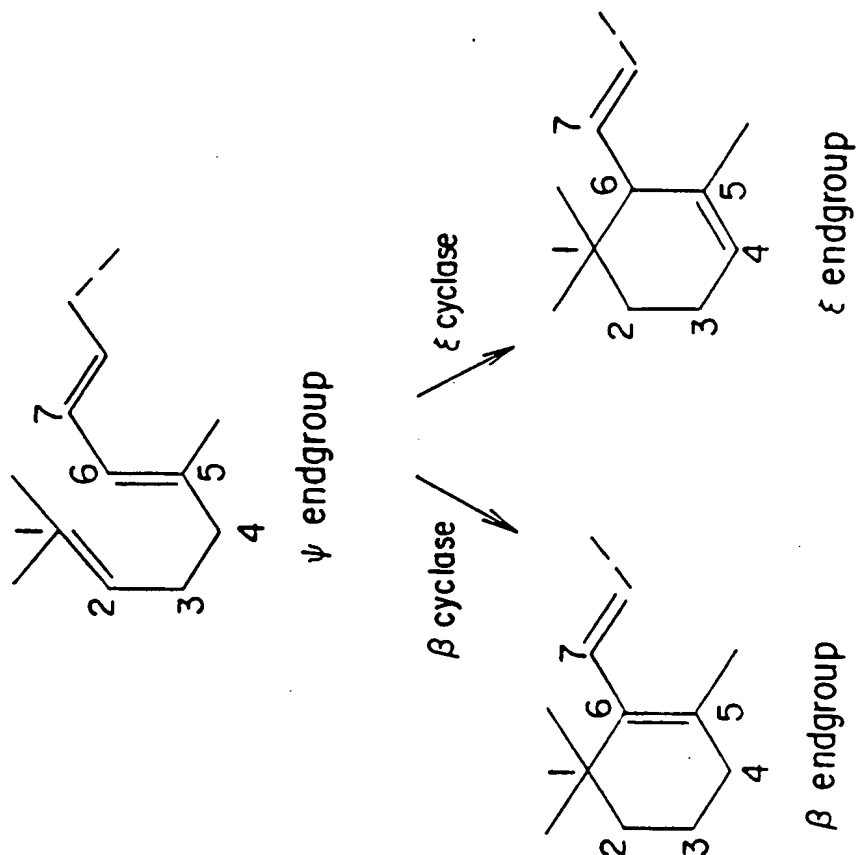


FIG. 2

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DRAFTSMAN			

FIG. 3



APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

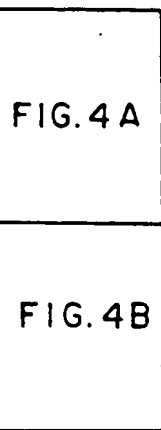


FIG. 4

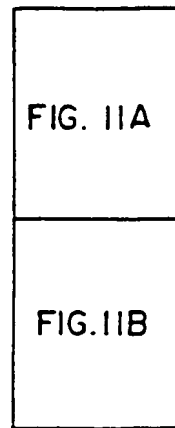


FIG. II

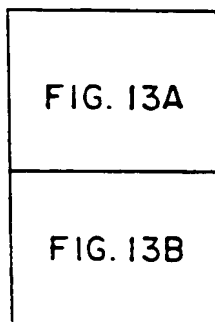


FIG. 13

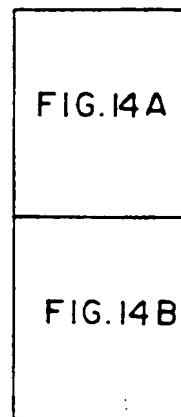


FIG. 14

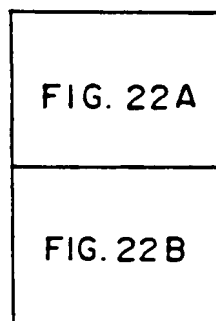


FIG. 22

## FIG. 4A

*Arabidopsis thaliana epsilon cyclase:*

1 acaaaaggaaataattag attcctctttctgcttgctataccttgaca 48  
 gaacaacataacaatggtgtaagtcttctc gctgtattcgaaattatttggaggaggaaac 108  
 atggagtgtgttggggctaggaatttcgca gcaatggcggtttcaacatttcggtcatgg 168  
 1 M E C V G A R N F A A M A V S T F P S W  
 agttgtcgaaggaaatttccagtggttaag agatacagctataggaatattcgcttcggt 228  
 21 S C R R K F P V V K R Y S Y R N I R F G  
 ttgtgtagtgtcagagctagcggcgccgga agttccggtagtgtgagagttgtgtagcgggtg 288  
 41 L C S V R A S G G G S S G S K S C V A V  
 agagaagatttcgctgacgaagaagatttt gcgaaagctggcggttctgagattctattt 348  
 61 R S D F A D E E D F V E A G G S R I L F  
 gttcaaatgcagcagaacaaagatatggat gaacagtctaagcttgttgataagttgcct 408  
 81 V Q M Q Q M K D M D S Q S K L V D K L P  
 cctatatcaactggtgatggtgctttggat catgtggttactggctgtggtcctgctggt 468  
 101 P I S I G D G A L D K V V I G C G P A G  
 ttagccttggctgcagaatcagctaagctt ggattaaaagttggactcattggtccagat 528  
 121 L A L A A K S A K L G L K V G L I G P D  
 cttccttttactaacaattacggtgtttgg gaagatgaattcaatgatcttgggctgcaa 588  
 141 L P F T M M Y G V M K D K F N D L G L G  
 aaatgtattgagcatgtttggagagagact attgcgacactggatgatgacaagcctatt 648  
 161 K C I K K V W R S T I V Y L D D D K P I  
 accattggccgtgcttatggaagagttagt cgacgtttgctccatgaggagcttttgagg 708  
 181 T I G R A Y G R V S R R L L X E E L L R  
 aggtgtgtcgagtcaagtggtctctgtacctt agctcgaaagttgacagcataacagaagct 768  
 201 R C V K S G V S Y L S S K V D S I T E A  
 tgtgatggccttagacttgttgcttgtgac gacaataacgtcattccctgcaggcttggc 828  
 221 S D G L X L V A C D D M M V I P C X L A  
 actgttgcttctggagcagcttcgggaaag ctcttgcaatacgaagttggtggacctaga 888  
 241 T V A S G A A S G K L L Q Y X V G G P R  
 gtctgtgcgcaaactgcatacggcgtggag gttgaggcggaaaatagtccatatgatcca 948

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## FIG. 4B

261 V C V Q T A Y G V X V X V X N S P Y D P  
 gatcaaatggttttcatggattacagagat tataactaacgagaaagttcggagcttagaa 1008  
 281 D Q M V P M D Y R D Y T M X X V R S L X  
 gctgagtatccaacgtttctgtacgccatg cctatgacaaagtcaagactcttcttcgag 1068  
 301 A K Y P T F L Y A M P M T K S R L F F K  
 gagacatgtttggcctcaaaagatgtcatg ccctttgatttgctaaaaacgaagctcatg 1128  
 321 K T C L A S K D V M P F D L L K T K L M  
 ttaagattagacacactcggaaattcgaatt ctaaagacttacgaagaggagtggctctat 1188  
 341 I P V G G S L P N T X Q K N L A F G A A  
 atcccagttggtggttccttgccaaacacc gaacaaaagaatctcgctttggtgctgcc 1248  
 361 I P V G G S L P M T X Q K N L A F G A A  
 gctagcatggtacatcccgcaacaggctat tcagttgtgagatctttgtctgaagctcca 1308  
 381 A S M V M P A T G Y S V V R S L S X A P  
 aaacatgcatcagtcacgcagagatacta agagaagagactaccaaacagattaacagt 1368  
 401 K Y A S V I A K I L R E E T T K Q I N S  
 aatatttcaagacaagcttaggatacttta tggccaccagaaaaggaaaagacagagagca 1428  
 421 M I S R Q A W D T L W P P E R X R Q R A  
 ttctttctctttggtcttgcaactcagagtt caattcgataccgaaggcattagaagcttc 1488  
 441 F F L F G L A L I V Q F D T X G I R S F  
 ttccgtactttcttcgccttccaaaatgg atgtggcaagggtttctaggatcaacatta 1548  
 461 F R T P F R L P K W M W Q G F L G S T L  
 acatcaggagatctcgttctctttgcttta tacatgttcgtcatttcaccaaacaatttg 1608  
 481 T S G D L V L F A L Y M P V I S P M M L  
 agaaaaggtctcattaatcatctcatctct gatccaaccggagcaaccatgataaaaacc 1668  
 501 R K G L I N W L I S D P T G A T M I K T  
 tatctcaaagtatgatttacttaccactc ttaggtttgtgtatatatatgccgatttat 1728  
 521 Y L K V  
 ctgaataatcgatcaaagaatggtatgtgg gttactaggaagttggaaacaaacacgtat 1788  
 agaatctaaggagtgatcgaaatggagacg gaaacgaaaagaaaaaatcagtcctttggt 1848  
 ccgtggctagtg 1868

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## FIG. 5

1 gctctttctc ctctctctct accgatttcc gactccgcct cccgaaatcc  
 51 ttatccggat tctctccgtc tcttcgattt aaacgctttt ctgtctgtta  
 101 cgtcgtcgaa gaacggagac agaattctcc gattgagaac gatgagagac  
 151 cggagagcac gagctccaca aacgctatag acgctgagta tctggcgttg  
 201 cgtttgccgg agaaattgga gaggaagaaa tcggagaggt ccacttatct  
 251 aatcgctgct atgttgctga gctttggtat cacttctatg gctgttatgg  
 301 ctgtttacta cagattctct tggcaaattg agggaggtga gatctcaatg  
 351 ttggaaatgt ttggtacatt tgctctctct gttggtgctg ctgttggtat  
 401 ggaattctgg gcaagatggg ctcatagagc tctgtggcac gcttctctat  
 451 ggaatatgca tgagtcacat cacaaaccaa gagaaggacc gtttgagcta  
 501 aacgatgttt ttgctatagt gaacgctggt ccagcgattg gtctcctctc  
 551 ttatggattc ttcaataaag gactcgttcc tggctctctgc tttggcgccg  
 601 ggtaggcat aacggtgttt ggaatcgctt acatgtttgt ccacgatggt  
 651 ctcgctgcaca agcgtttccc tgtaggtccc atcgccgacg tcccttacct  
 701 ccgaaaggtc gccgccgctc accagctaca tcacacagac aagttcaatg  
 751 gtgtaccata tggactgttt cttggaccca aggaattgga agaagttgga  
 801 ggaaatgaag agttagataa ggagattagt cggagaatca aatcatacaa  
 851 aaaggcctcg ggctccgggt cgagttcgag ttcttgactt taaacaagtt  
 901 ttaaatccca aattcttttt ttgtcttctg tcattatgat catcttaaga  
 951 cggtct

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## FIG. 6

64

SFSS SSTDFRLRLP KSLSGFSPSL RFRKFSVCYV VEERRQNSPI ENDERPESTS STNAIDAAYL

A.thal.

144

ALRLAEKLER KKSERSTYLI AAMLSSFGIT SMAMAVYYR FSWQMEGGEI SMLEMGITFA LSVGAAGVME FWARWAHRAL  
 ..... MTOFL IWWATVLVME LTAYSVHRWI  
 ..... MTNFI IWWATVLVME LTAYSVHRWI  
 ..... ML.NSL IVILSVIAME GIAAFTHRYI  
 ..... MLWTNAL IVITVIGME VIAALAHKYI  
 ..... f -v-----ME --A---Hr--

A.thal.  
 A.alcal.  
 A.aurant.  
 E.herb.  
 E.ured.  
 Consensus

Predicted TM helix

Predicted TM helix

WHASL.NMH ESHHKPREGP FELNDVFAIV NAGPAIGLLS YGFENKGLVP GLCFGAGLGI TVFGIAYMFV HDGLVHKRFP  
 MGPLGwGH KSHHEHDHA LEKNDLYGW FAVLATILFT VGAYWwPVLW WI....ALGM TVYGLIYFIL HDGLVHORWP  
 MGPLGwGH KSHHEHDHA LEKNDLYGLV FAVIATVLEF VGIWwPVLW WI....ALGM TVYGLIYFVL HDGLVHORWP  
 MG.WGwRH ESHHTPRKGV FKLNDLFAW FAGVAIALIA VGTAGWwPLO WI....GCGM TVYGLLYFLV HDGLVHORWP  
 MG.WGwGH LSHHEPRKGA FEVNDLYAW FAALSILLIY LGSTGwPPLQ WI....GAGM TAYGLLYFMV HDGLVHORWP  
 -H--l-W--H -SHH-pr-g- fE-ND--a-V -A--ai-L-- -G-----glG-- Tv-G--Y--v HDGLVH-R-P

A.thal.  
 A.alcal.  
 A.aurant.  
 E.herb.  
 E.ured.  
 Consensus

Predicted TM helix

Predicted TM helix

VGPIADVPYL RKVAAHQH HT..DKFNGV PYGLFLGPKE LEEVGGNEEL DKEISRRIKS YKASGSGSS SSS\*...  
 FRYIPRGYF RRLYQAHRLH HAVEGRDHCV SEGFIYAPP. VDKLKQDLKR SGVLRPODER PS\*.....  
 FRYIPRKGVA RRLYQAHRLH HAVEGRDHCV SEGFIYAPP. VDKLKQDLKM SGVLRPAEAOE RT\*.....  
 FRYIPRGGYL KRLYVAHRLH HAVRGREGCV SEGFIYARK. PADLOATLRE RHGRPPKRDA AKDRPDAASP SSSSPE\*  
 FRYIPRGGYL KRLYMAHRLH HAVRGKEGCV SEGFIYAPP. LSKLQATLRE RHG..ARAGA ARDAQGGEDE PASGK\*.  
 ---l----Yl r-----AH-lH H-----V --G----p-----S-----

A.thal.  
 A.alcal.  
 A.aurant.  
 E.herb.  
 E.ured.  
 Consensus



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## FIG. 7

1 ccacgggtcc gcctccccgt ttttttccga tccgatctcc ggtgccgagg  
 51 actcagctgt ttgttcgcgc tttctcagcc gtcaccatga ccgattctaa  
 101 cgatgctgga atggatgctg ttcagagacg actcatgttt gaagacgaat  
 151 gcattctcgt tgatgaaaat aatcgtgtgg tgggacatga cactaagtat  
 201 aactgtcatc tgatggaaaa gattgaagct gagaattttac ttcacagagc  
 251 tttcagtggtg tttttattca actccaagta tgagttgctt ctccagcaac  
 301 ggtcaaaaac aaaggttact tttccacttg tgtggacaaa cactttgttg  
 351 agccatcctc tttaccgtga atccgagctt attgaagaga atgtgcttgg  
 401 tgtaagaaat gccgcacaaa ggaagctttt cgatgagctc ggtattgtag  
 451 cagaagatgt accagtcgat gagttcactc ccttgggacg catgctttac  
 501 aaggcacctt ctgatgggaa atggggagag cacgaagttg actatctact  
 551 cttcatcgtg cgggatgtga agcttcaacc aaaccagat gaagtggctg  
 601 agatcaagta cgtgagcagg gaagagctta aggagctggt gaagaaagca  
 651 gatgctggcg atgaagctgt gaaactatct ccatggttca gattgggtgt  
 701 ggataatttc ttgatgaagt ggtgggatca tgttgagaaa ggaactatca  
 751 ctgaagctgc agacatgaaa accattcaca agctctgaac tttccataag  
 801 ttttggatct tccccctccc ataataaaat taagagatga gacttttatt  
 851 gattacagac aaaactggca acaaaatcta ttcttaggat tttttttg  
 901 tttttattta cttttgatc atctctagtt tagttttcat cttaaaaaaa  
 951 aaaa

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O. G. H. 3	CLASS	SUBCLASS

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	CLASS	

## FIG. 8

1 caccaatgtc tgtttcttct ttatttaatc tcccattgat tgcctcaga  
51 tctctcgtc ttcgtcttc tttttcttct ttccgatttg cccatcgctcc  
101 TCTGTCATCG ATTCACCGA GAAAGTTACC GAATTTTCGT GCTTTCTCTG  
151 GTACCGCTAT GACAGATACT AAAGATGCTG GTATGGATGC TGTTCAGAGA  
201 CGTCTCATGT TTGAGGATGA ATGCATTCTT GTTGATGAAA CTGATCGTGT  
251 TGTGGGGCAT GTCAGCAAGT ATAATTGTCA TCTGATGGAA AATATTGAAG  
301 CCAAGAATTT GCTGCACAGG GCTTTTAGTG TATTTTTATT CAACTCGAAG  
351 TATGAGTTGC TTCTCCAGCA AAGGTCAAAC ACAAAGGTTA CGTTCCCTCT  
401 AGTGTGGACT AACACTTGTT GCAGCCATCC TCTTTACCGT GAATCAGAGC  
451 TTATCCAGGA CAATGCACTA GGTGTGAGGA ATGCTGCACA AAGAAAGCTT  
501 CTCGATGAGC TTGGTATTGT AGCTGAAGAT GTACCAGTCG ATGAGTTCAC  
551 TCCCTTGGGA CGTATGCTGT ACAAGGCTCC TTCTGATGGC AAATGGGGAG  
601 AGCATGAACT TGATTACTTG CTCTTCATCG TCGAGACGT GAAGGTTCAA  
651 CCAAACCCAG ATGAAGTAGC TGAGATCAAG TATGTGAGCC GGAAGAGCT  
701 GAAGGAGCTG GTGAAGAAAG CAGATGCAGG TGAGGAAGGT TTGAAACTGT  
751 CACCATGGTT CAGATTGGTG GTGGACAATT TCTTGATGAA GTGGTGGGAT  
801 CATGTTGAGA AAGGAACTTT GGTGAAGCT ATAGACATGA AAACCATCCA  
851 CAAACTCTGA ACATCTTTTT TTAAAGTTTT TAAATCAATC AACTTTCTCT  
901 TCATCATTTT TATCTTTTCG ATGATAATAA TTTGGGATAT GTGAGACACT  
951 TACAAAACCT CCAAGCACCT CAGGCAATAA TAAAGTTTGC GGCCGC

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## FIG. 9

1 CTCGGTAGCT GGGCACAATC GCTATTTGGA ACCTGGCCCCG GCGGCAGTCC  
 51 GATGCCGCGA TGCTTCGTTT GTTGCTCAGA GGCCTCAGGC ATATCCCCCG  
 101 CGTGAACTCC GCCCAGCAGC CCAGCTGTGC ACACGCGCGA CTCCAGTTTA  
 151 AGCTCAGGAG CATGCAGATG ACGCTCATGC AGCCCAGCAT CTCAGCCAAT  
 201 CTGTCGCGCG CCGAGGACCG CACAGACCAC ATGAGGGGTG CAAGCACCTG  
 251 GGCAGGCGGG CAGTCGCAGG ATGAGCTGAT GCTGAAGGAC GAGTGCATCT  
 301 TGSTGGATGT TGAGGACAAC ATCACAGGCC ATGCCAGCAA GCTGGATGTG  
 351 CACAAGTTCC TACCACATCA GCCTGCAGGC CTGCTGCACC GGGCCTTCTC  
 401 TGTGTTCTTG TTTGACGATC AGGGGCGACT GCTGCTGCAA CAGCGTGCC  
 451 GCTCAAAAAT CACCTTCCCA AGTGTGTGGA CGAACACCTG CTGCAGCCAC  
 501 CCTTTACATG GGCAGACCCC AGATGAGGTG GACCAACTAA GCCAGGTGGC  
 551 CGACGGAACA GTACCTGGCG CAAAGGCTGC TGCCATCCGC AAGTTGGAGC  
 601 ACGAGCTGGG GATACCAGCG CACCAGCTGC CGGCAAGCGC GTTTCGCTTC  
 651 CTCACGCGTT TGCCTACTG TGCCGCGGAC GTGCAGCCAG CTGCGACACA  
 701 ATCAGCGCTC TGGGGCGAGC ACGAAATGGA CTACATCTTG TTCATCCGGG  
 751 CCAACGTCAC CTTGGCGCCC AACCCTGACG AGGTGGACGA AGTCAGGTAC  
 801 GTGACGCAAG AGGAGCTGCG GCAGATGATG CAGCCGGACA ACGGGCTGCA  
 851 ATGGTCGCGG TGGTTTCGCA TCATCGCCGC GCGCTTCCTT GAGCGTTGGT  
 901 GGGCTGACCT GGACGCGGCC CTAAACACTG ACAAACACGA GGATTGGGGA  
 951 ACGGTGCATC ACATCAACGA AGCGTGAAAG CAGAAGCTGC AGGATGTGAA  
 1001 GACACGTCAT GGGGTGGAAT TGCCTACTTG GCAGCTTCGT ATCTCCTTTT  
 1051 TCTGAGACTG AACCTGCAGT CAGGTCCAC AAGGTCAGGT AAAATGGCTC  
 1101 GATAAAATGT ACCGTCACCT TTTGTCGCGT ATACTGAACT CCAAGAGGTC  
 1151 AAAAAAAAAA AAAAA

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	CLASS	

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## FIG. 10

1 CTCGGTAGCT GGCCACAATC GCTATTTGGA ACCTGGCCCC GCGGCAGTCC  
 51 GATGCCGCGA TGCTTEGTTT GTTGCTCAGA GGCCTCACGC ATATCCCCGC  
 101 CGTGAACTCC GCCCAGCAGC CCAGCTGTGC ACACGCGCGA CTCCAGTTTA  
 151 AGCTCAGGAG CATGCAGCTG CTTTCCGAGG ACCGCACAGA CCACATGAGG  
 201 GGTGCAAGCA CCTGGGCAGG CGGGCAGTCG CAGGATGAGC TGATGCTGAA  
 251 GGACGAGTGC ATCTTGGTAG ATGTTGAGGA CAACATCACA GGCCATGCCA  
 301 GCAAGCTGGA GTGTCACAAG TTCCTACCAC ATCAGCCTGC AGGCCTGCTG  
 351 CACCGGGCCT TCTCTGTGTT CCTGTTTGAC GATCAGGGGC GACTGCTGCT  
 401 GCAACAGCGT GCACGCTCAA AAATCACCTT CCCAAGTGTG TGGACGAACA  
 451 CCTGCTGCAG CCACCCTTTA CATGGGCAGA CCCCAGATGA GGTGGACCAA  
 501 CTAAGCCAGG TGGCCGACGG AACAGTACCT GGCGCAAAGG CTGCTGCCAT  
 551 CCGCAAGTTG GAGCAGGAGC TGGGGATACC AGCGCACCAG CTGCCGCGAA  
 601 GCGCGTTTCG CTTCTCAGC CGTTTGCACT ACTGTGCCCC GGACGTGCAG  
 651 CCAGCTGCGA CACAATCAGC GCTCTGGGGC GAGCAGGAAA TGGACTACAT  
 701 CTTGTTTCATC CGGGCCAACG TCACCTTGGC GCCCAACCCT GACGAGGTGG  
 751 ACCAAGTCAG GTACGTGACG CAAGAGGAGC TGCGGCAGAT GATGCAGCCC  
 801 GACAACGGGC TTCAATGGTC GCGGTGGTTT CGCATCATCG CCGCGCGCTT  
 851 CCTTGAGCGT TGGTGGGCTG ACCTGGACGC GGCCCTAAAC ACTGACAAAC  
 901 ACGAGGATTG GGGAACGGTG CATCACATCA ACGAAGCGTG AAGGCAGAAG  
 951 CTGCAGGATG TGAAGACACG TCATGGGGTG GAATTGCGTA CTTGGCAGCT  
 1001 TCGTATCTCC TTTTCTGAG ACTGAACCTG CAGAGCTAGA GTCAATGGTG  
 1051 CATCATATTC ATCGTCTCTC TTTTGTTTTA GACTAATCTG TAGCTAGAGT  
 1101 CACTGATGAA TCCTTTACAA CTTTCAAAAA AAAAA

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## FIG. 11A

1	HP04	MLRSLLRGLT	HIPRVNSAQQ	PSCAHARLQF	KLRSMQMTLM	QPSISANLSR	50
	HP05	MLRSLLRGLT	HIPRVNSAQQ	PSCAHARLQF	KLRSMQLL..	.....	
	ATDP7	MSVSSLFNLP	.LIRLRLSLA.	LSSSFSSFRF	AHRPLSSIS.	PRKLPNFRAF	
	C.brew.	MS.SSMLNFT	.ASRIVSLPL	LSSPPSRVHL	PLCFFSPISL	TQRFSAKLTF	
	ATOP5	.....	.TGPPPRFFP	IRSPVPRTQL	FVRAFSAV..	.....	
	S.cerev.	..MTADNNSM	PHGAVSSYAK	LVQNQTPEDI	LEEFPEIIPL	QQRPN...TR	

51	AEDRTDHMRG	ASTWAGGQSQ	DELMLKDECI	LVDVEDNITG	HASKLECHKF	100
	SEDRTDHMRG	ASTWAGGQSQ	DELMLKDECI	LVDVEDNITG	HASKLECHKF	
	S..GTA.MTD	TKDAGMDAVQ	RRLMFEDECI	LVDETDRVVG	HVSKYNCHLM	
	SSQATT.MGE	VVDAGMDAVQ	RRLMFEDECI	LVDENDKVVG	HESKYNCHLM	
	.....T.MTD	SNDAGMDAVQ	RRLMFEDECI	LVDENNRVVG	HDTKYNCHLM	
	SSETSNDESG	ETCFSGHDEE	QIKLMNENCI	VLDWDDNAIG	AGTKKVCHLM	

101	LPHQPAGLLH	RAFSVFLFDD	QGRLLLQORA	RSKITFPSVW	TNTCCSHPLH	150
	LPHQPAGLLH	RAFSVFLFDD	QGRLLLQORA	RSKITFPSVW	TNTCCSHPLH	
	ENIEAKNLLH	RAFSVFLFNS	KYELLLOQRS	NTKVTFPLVW	TNTCCSHPLY	
	ENIESENLLH	RAFSVFLFNS	KYELLLOQRS	ATKVTFPLVW	TNTCCSHPLY	
	EKIEAENLLH	RAFSVFLFNS	KYELLLOQRS	KTKVTFPLVW	TNTCCSHPLY	
	ENIE.KGLLH	RAFSVFIFNE	QGELLLOQRA	TEKITFPDLW	TNTCCSHPLC	

151	GQTPDEVDQL	SQVADGTVPG	AKAAAIRKLE	HELGI PAHQL	PA.SAFRFLT	200
	GQTPDEVDQL	SQVADGTVPG	AKAAAIRKLE	HELGI PAHQL	PA.SAFRFLT	
	RE.....	SELIQDNALG	VRNAAQRKLL	DELGIVAEDV	PV.DEFTPLG	
	RE.....	SELIDENCLG	VRNAAQRKLL	DELGI PAEDL	PV.DQFIPLS	
	RE.....	SELIEENVLG	VRNAAQRKLF	DELGIVAEDV	PV.DEFTPLG	
	ID...DELGL	KGKLDDKIKG	AITAAVRKLD	HELGIPEDET	KTRGKFHFLN	

201	RLHYCAADVQ	PAATQSALWG	EHEMDYILFI	....RANVTL	APNPDEVDEV	250
	RLHYCAADVQ	PAATQSALWG	EHEMDYILFI	....RANVTL	APNPDEVDEV	
	RMLY.....	.KAPSDGKWG	EHELDYLLFI	....VRDVKV	QPNPDEVAEI	
	RILY.....	.KAPSDGKWG	EHELDYLLFI	....IRDVNL	DPNPDEVAEV	
	RMLY.....	.KAPSDGKWG	EHEVDYLLFI	....VRDVKL	QPNPDEVAEI	
	RIHY.....	.MAPSNEPWG	EHEIDYILFY	KINAKENLTV	NPNVNEVRDF	

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## FIG. 11B

251				300
RYVTQEELRQ	MMQ....PDN	GLQWSPWFRI	IAARFLERWW	ADLDAALNTD
RYVTQEELRQ	MMQ....PDN	GLQWSPWFRI	IAARFLERWW	ADLDAALNTD
KYVSREELKE	LVKKADAGEE	GLKLSPWFRL	VVDNFLMKWW	DHVEKGTIVE
KYMNRRDDLKE	LLRKADAE	GVKLSPWFRL	VVDNFLFKWW	DHVEKGSLKD
KYVSREELKE	LVKKADAGDE	AVKLSPWFRL	VVDNFLMKWW	DHVEKGTITE
KWVSPNDLKT	MF.....ADP	SYKFTPWFKI	ICENYLFNWW	EQLDDLSEVE

301

KHEDWGTVHH INEA\*

KHEDWGTVHH INEA\*

A.IDMKTIHK L\*

A.ADMKTIHK L\*

A.ADMKTIHK L\*

A.ADMKTIHK L\*

NDRQ...IHR ML\*

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## FIG. 12

1 ccaaaaacaa ctcaaattct ctcggtcgct cttactccgc catgggtgac  
 51 gactccggca tggatgctgt tcagcgacgt ctcattgtttg acgatgaatg  
 101 cattttgggtg gatgagtgtg acaatgtggt gggacatgat accaaataca  
 151 attgtcactt gatggagaag attgaaacag gtaaaatgct gcacagagca  
 201 ttcagcgcttt ttctattcaa ttcaaaatac gagttacttc ttcagcaacg  
 251 gtctgcaacc aaggtgacat ttcttttagt atggaccaac acctgttgca  
 301 gccatccact ctacagagaa tccgagcttg ttcccgaac gcctgagaga  
 351 atgctgcaca gaggaxxxxx xxxxxxxxxxxx xxxxxxxxxxxx  
 401 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx  
 451 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx  
 501 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx  
 551 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx  
 601 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx  
 651 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx tcatgtgcaa aagggtagac  
 701 tcaactgaatg caatttgata tgaaaaccat acacaagctg atatagaaac  
 751 acaccctcaa ccgaaaagca agcctaataa ttcgggttgg gtcgggtcta  
 801 ccatcaattg tttttttctt ttaacaactt ttaattctta tttgagcatg  
 851 ttgattcttg tcttttggtg gtaagatttt ggggttcgtt tcagttgtaa  
 901 taatgaacca ttgatgggtt gcaatttcaa gtccctatcg acatgtagtg  
 951 atctaaaaaa

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 13A

1	Plant beta A.t. epsilon Consensus	.....MDTLLKT PN-LaF1-p- -HG.....F- MECVGARNFA AMAVSTFPSW SCRRKFPVVK RYSYRNIRFG -----F-----F-----F-----	70 CS--g---VC REDFADEXDF -E-----
71	Plant beta A.t. epsilon Consensus	Cyanobacterial enzyme begins → VV--SsALLa LVPETKKKNI DFELPmYDp. S.Kg-VV VKAGGSEIL FVQMQQNKDM DEQSKLVVDKL PPISIGDGA VK---S--L- -V-----D-----D-----S-----	140 DLAVVGGGPA GLAVAQQVSE AGLSVcSIDp DHVVICGPA GLALAAESAK LGLKVGLIGP D--V-G-GPA GLA-A-----GL-V--I-P- ↑
		Possible subunit interaction domain	Dinucleotide-binding signature
141	Plant beta A.t. epsilon Consensus	.-PKLIWPNN YGVWVDEFEA MDLLDCLDaT WSGa-VYiDd DLP...FTNN YGVWDEDFND LGLQKCIHV WRETIVYLD --P-----NN YGVW-DEF-- --L--C-----W-----VY-DD	210 KMKQKCI-NG ELLRRCVESG -----C-----R-Y GRV-R--L--
211	Plant beta A.t. epsilon Consensus	VKFHgaKvik ViHE.E-kSm liCnDG-tIQ AtVVLDA VSYLSSKVDs ITKASDGLRL VACDDNNVIP CRLATV V-----KV-- ----- --C-D---I- -----A-G-	280 YGILAEVeeh YGVEVEVENS -----Q-A YG-----gv-
		Conserved region #1	



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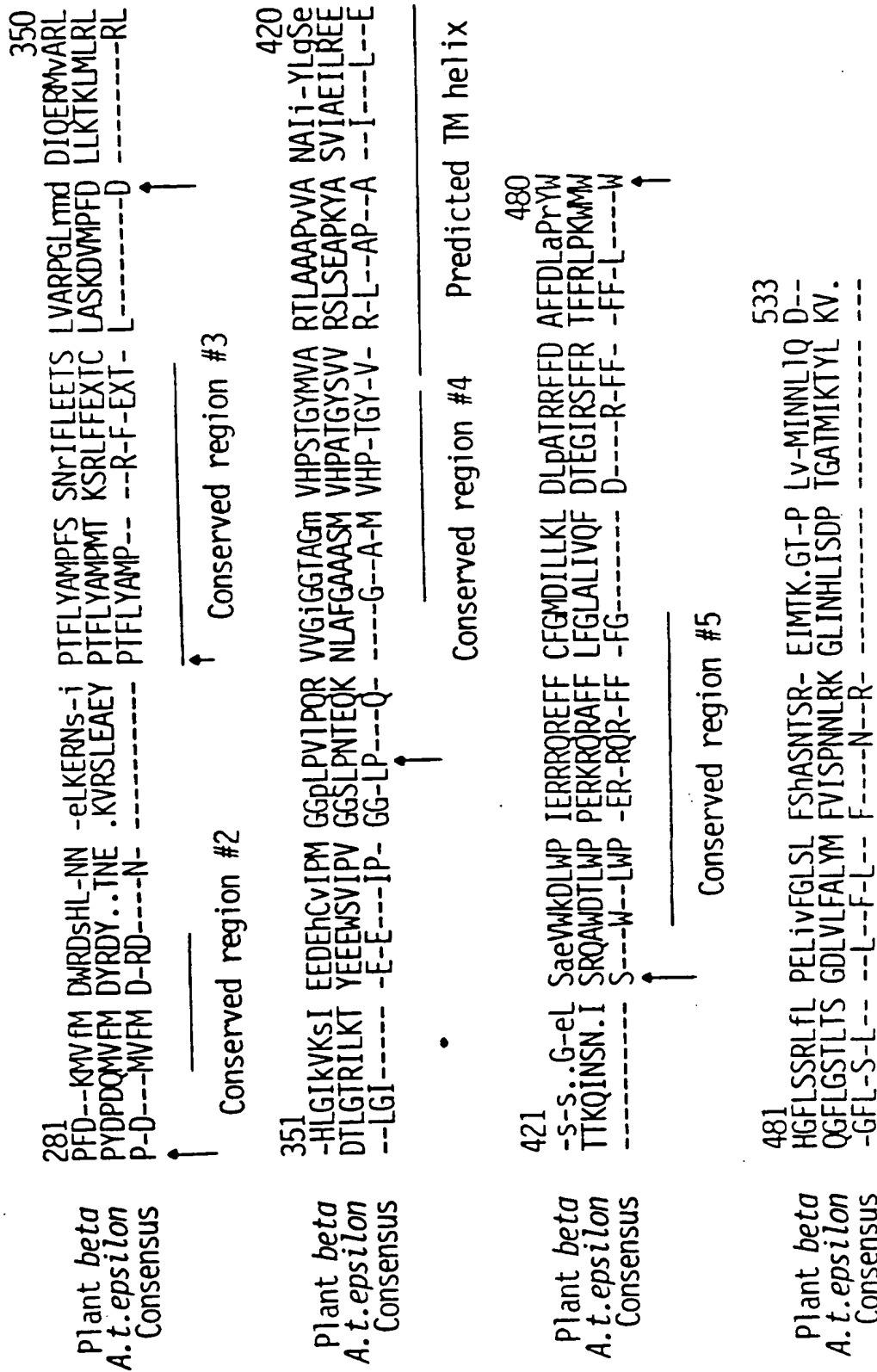


FIG. 13B

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## FIG. 14A

*Adonis palaestina*  $\varepsilon$ -cyclase cDNA #5

Length: 1898

1	aaaggagtgt	tctattaatg	ttactgtcgc	attcttgcaa	cacttatatt
51	caaactccat	tttcttcttt	tctcttcaaa	acaacaaact	aatgtgagca
101	gagtatctgg	ctatggaact	acttggtgtt	cgcaacctca	tctcttcttg
151	ccctgtgtgg	acttttggaa	caagaaacct	tagtagttca	aaactagctt
201	ataacataca	tcgatatggt	tcttcttgta	gagtagattt	tcaagtgaga
251	gctgatggtg	gaagcgggag	tagaagttct	gttgcttata	aagagggttt
301	tgtggatgaa	gaggatttta	tcaaagctgg	tggttctgag	cttttgtttg
351	tccaaatgca	gcaaacaaag	tctatggaga	aacaggccaa	gctcgccgat
401	aagttgccac	caataccttt	tggagaatcc	gtgatggact	tggttgtaat
451	aggttgtgga	cctgctggtc	tttactggc	tgcagaagct	gctaagctag
501	ggttgaaagt	tggccttatt	ggtcctgac	ttccttttac	aaataattat
551	ggtgtgtggg	aagacgagtt	caaagatctt	ggacttgaac	gttgatcga
601	gcatgcttgg	aaggacacca	tcgtatatct	tgataatgat	gctcctgtcc
651	ttattggtcg	tgcatatgga	cgagttagtc	gacatttgct	acatgaggag
701	ttgctgaaaa	ggtgtgtgga	gtcagggtga	tcatatctgg	attctaaagt
751	ggaaaggatc	actgaagctg	gtgatggcca	tagccttgta	gtttgtgaaa
801	atgagatctt	tatcccttgc	aggcttgcta	ctgttgcac	tggagcagct
851	tcagggaaac	ttttggagta	tgaagtaggt	ggccctcgtg	tttgtgtcca
901	aaccgcttat	ggggtggagg	ttgaggtgga	gaacaatcca	tacgatccca
951	acttaatggt	attcatggac	tacagagact	atatgcaaca	gaaattacag
1001	tgctcggaag	aagaatatcc	aacatttctC	tatgtcatgc	ccatgtcgcc
1051	aacaagactt	ttttttgagg	aaacctgttt	ggcctcaaaa	gatgccatgc
1101	cattcgatct	actgaagaga	aaactgatgt	cacgattgaa	gactctgggt
1151	atccaagtta	caaaagttta	tgaagaggaa	tggatcatata	ttcctgttgg
1201	tggttcttta	ccaaacacag	agcaaaagaa	cctagcattt	ggtgctgcag
1251	caagcatggt	gcatccagca	acaggctatt	cggttgtagc	gtcactgtca
1301	gaagctccaa	aatatgcttc	tgtaattgca	aagattttga	agcaagataa
1351	ctctgcgtat	gtggtttctg	gacaaagtag	tgcagtaaac	atttcaatgc
1401	aagcatggag	cagtctttgg	ccaaaggagc	gaaaacgtca	aagagcatTc
1451	tttcttttTg	gattagagct	tattgtgcag	ctagatattg	aagcaaccag
1501	aacattcttt	agaaccttct	tccgcttgcc	aacttggatg	tgggtgggtt
1551	tccttgggtc	ttcactatca	tctttcgatc	tcgtcttggt	ttccatgtac
1601	atgtttgttt	tggcgccaaa	cagcatgagg	atgtcacttg	tgagacattt
1651	gctttcagat	ccttctggtg	cagttatggt	aagagcttac	ctcgaaaggt
1701	agtctcatct	attattaaac	tctagtgttt	caccaaataa	atgaggatcc
1751	ttcgaatgtg	tatatgatca	tctctatgta	tatcctgtac	tctaattctca
1801	taaagtaaat	gccgggtttg	atattgttgt	gtcaaaccgg	ccaatgatat
1851	aaagtaaatt	tattgataca	aaagtagttt	ttttccttaa	aaaaaaaa

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## FIG. 14B

*Adonis palaestina*  $\epsilon$ -cyclase #5 predicted polypeptide  
 TRANSLATE from: 113 to: 1702 Length: 529 amino acids

1	MELLGVRNLI	SSCPWTFGT	RNLSSSKLAY	NIHRYGSSCR	VDFQVRADGG
51	SGSRSSVAYK	EGFVDEEDFI	KAGGSELLFV	QMQQTKSMEK	QAKLADKLPP
101	IPFGESVMDL	VVIGCGPAGL	SLAAEAAKLG	LKVGLIGPDL	PFTNNYGVWE
151	DEFKDLGLER	CIEHAWKDTI	VYLDNDAPVL	IGRAYGRVSR	HLLHEELLKR
201	CVESGVSYLD	SKVERITEAG	DGHSLVVCEN	EIFIPCRLAT	VASGAASGKL
251	LEYEVGGPRV	CVQTAYGVEV	EVENNPYDPN	LMVFMDYRDY	MQQKLOCSEE
301	EYPTFLYVMP	MSPTLFFEE	TCLASKDAMP	FDLLKRKLMS	RLKTLGIQVT
351	KVYEEWSYI	PVGGS LPNTE	QKNLAFGAAA	SMVHPATGYS	VVRSLSEAPK
401	YASVIKILK	QDNSAYVVS	QSSAVNISMQ	AWSSLWPKER	KRQRAFFLFG
451	LELIVQLDIE	ATRTFFRTFF	RLPTWMWGF	LGSSLSSF DL	VLFSMYMFVL
501	APNSMRMSLV	RHLLSDPSGA	VMVRAYLER*		

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## FIG. 15A

DNA sequence of potato cDNA (GenBank R27545) obtained from Nicholas J. Provart

potato.seq Length: 1378 August 2, 1996 13:06 Type: N Check: 605 ..

```

1 tagcggnnnn naggatgagt tcaaagatct tggctctcaa gcctgcattg
51 aacatgtttg gcgggatacc attgtatata ttgatgatga tgatcctatt
101 cttattggcc gtgcctatgg aagagttagt cgccatttac tgcacgagga
151 gttactcaaa aggtgtgtgg aggcaggtgt tttgtatcta aactcgaaag
201 tggataggat tgttgaggcc acaaatggcc acagtcttgt agagtgcgag
251 ggtgatgttg tgattccctg caggtttgtg actggttgcg cgggagcagc
301 ctcggggaaa ttcttgagcgt atgagttggg aggtcctaga gtttctgttc
351 aaacagctta tggagtggaa gttgaggtcg ataacaatcc atttgacccg
401 agcctgatgg ttttcatgga ttatagagac tatgtcagac acgacgtca
451 atctttagaa gctaaatata caacatttct ctatgccatg cccatgtctc
501 caacacgagt ctttttcgag gaaacttgtt tggcttcaaa agatgcaatg
551 ccattcgatc tgtaaagaa aaaattgatg ttacgattga acaccctcgg
601 tgtaagaatt aaagaaattt atgaggagga atggtcttac ataccagttg
651 gaggatcttt gccaaatata gaacaaaaaa cacttgcat tgggtgctgct
701 gctagcatgg ttcatccagc cacaggttat tcagtcgtca gatcactgtc
751 tgaagctcca aaatgcgcct tcgtgcttgc aaatatatta cgacaaaatc
801 atagcaagaa tatgcttact agttcaagta ccccgagtat ttcaactcaa
851 gcttgaaca ctctttggcc acaagaacga aaacgacaaa gatcgttttt
901 cctatttga ctggctctga tattgcagct ggatattgag gggataaggt
951 catttttccg cggttcttc cgtgtgccaa aatggatgtg gcagggattt
1001 cttggttcaa gtctttctn agcagacctc atgttatttg ctttctacat
1051 gtttattatt gcaccaaag acatgagaag aggcttaatc agacatcttt
1101 tatctgatcc tactggtgca acattgataa gaacttatct tacattttag
1151 agtaaattcc tcctacaata gttgttgaan nagaggcctc attacttcag
1201 attcataaca gaaatcgcg tctctcgagg ccttgatat aacattttca
1251 ctaggttaat attgcttgaa taagttgcac agtttcagtt tttgtatctg
1301 cttctttttt gtccaagatc atgtattgan ccaatttata tacattgccca
1351 gtatatataa attttataaa aaaaaaaaa

```

poteps.pep Length: 378 TRANSLATE from: 14 to: 1147

```

1 DEFKDLGLQA CIEHVWRDTI VYLDLDDPIL IGRAYGRVSR HLLHEELLKR
51 CVEAGVLYLN SKVDRIVEAT NGHSLVECEG DVVIPCRFVT VASGAASGKF
101 LQYELGGPRV SVQTAYGVEV EVDNNPFDPS LMVFM DYRDY VRHDAQSLEA
151 KYPTFLYAMP MSPTRVFFEE TCLASKDAMP FDLLKKKML RLNTLGVRIR
201 EIYEEWSYI PYGGS LPNTE QKTALFGAAA SMVHPATGYS VVRSLSEAPK
251 CAFVLNLR QNHSKNMLTS SSTPSISTQA WNTLWPQERK RQRSFFLFLGL
301 ALILQLDIEG IRSFFRAFFR VPKWMWQGFL GSSLXADLM LFAFYMFIIA
351 PNDMRRGLIR HLLSDPTGAT LIRTYLTF*

```

## FIG. 15B

Chimeric lettuce/potato lycopene  $\epsilon$ -cyclase: converts lycopene to  $\delta$ -carotene, the lettuce cDNA converts lycopene to  $\epsilon$ -carotene and the potato cDNA does not produce an active enzyme

(amino acids in lower case are from lettuce and those in uppercase are from the potato cDNA; an *Ava*II site in common to the two cDNAs was used to construct the chimera)

```

1  mecfgarnmt atmavftcpt ftdcnirhkf sllkqrrftn lsassslrqi
51  kcsaksdrcv vdkqgisvac eedyvkaggs elffvqmqrt ksmesqskls
101 eklaqipign cildlvvigc gpaglalaee saklglnvgl igpdlpftnn
151 ygvwqdefig lglegciehs wkdtlvyldd adpirigray grvhrdlhe
201 ellrrcvesg vsylsskver iteapngysl iecegnitip crlatvasga
251 asgkfleyel gGPRVSVQTA YGVEVEVDNN PFDPSLMVFM DYRDYVRHDA
301 QSLEAKYPTF LYAMPMSPTR VFFEETCLAS KDAMPFDLLK KKLMLRLNTL
351 GVRIKEIYEE EWSYIPVGGs LPNTEQKTLA FGAAASMVHP ATGYSVVRSL
401 SEAPKCAFVL ANILRQNHsk NMLTSSSTPS ISTQAWNTLW PQERKRQRSF
451 FLFGLALILQ LDIEGIRSFF RAFFRVPKWM WQGFLGSSLS XADLMLFAFY
501 MFIIAPNDMR RGLIRHLLSD PTGATLIRTY LTF*

```

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## FIG. 16

GAP comparison of Arabidopsis  $\epsilon$ -cyclase x potato  $\epsilon$ -cyclase (partial)

blosum62.cmp Gap Weight: 12 Average Match: 2.912

Length Weight: 4      Average Mismatch: -2.003

Quality: 1485 Length: 529

Ratio: 3.929 Gaps: 1

Percent Similarity: 79.893    Percent Identity: 76.139

Match display thresholds for the alignment(s):

$$I = \text{IDENTITY} \quad : = 2 \quad . = 1$$

151 EDEFNDLGLQKCIHVWRETIVYLDDDKPITIGRAYGRVSRLLHEELLR 200

1 .DEFKDLGLQACIEHVWRDTIVYLDDDDPILIGRAYGRVSRHLLHEELLK 49

201 RCVESGVSYLSSKVDSITEASDGLRLVACDDNNVIPCRLATVASGAASGK 250

50 RCVEAGVLYLNSKVDRIVEATNGHSLVECEGDVVIPCRFVTVASGAASGK 99

251 LLQYEVGGPRVCVQTAYGVÈVEVENSPYDPDQMFMDYRDYTNEKVRSLÈ 300

100 FLQYELGGPRVSVQTAYGVEVEVDNNPFDPSLMVEMDYRDYVRHDAQSLE 149

301 AEYPTFLYAMPMTKSRLFFEETCLASKDVMPFDLLKTKMLRLDTLGIRI 350

150 AKYPTFLYAMPMSPTRVFFETCLASKDAMPFDLLKKKLMLRLNTLGVRI 199

351 LKTYEEEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGYSVVRSLSEAP 400

200 KEIYEEESYIPVGGSLPNTQKTLAFGAAASMVHPATGYSVVRSLSEAP 249

401 KYASVIAEILREETTKQI.....NSNISRQAWDTLWPPERKRQRAFFFLFG 445

250 KCAFVLANILRONHSKNMLTSSSTPSISTQAWNTLWPQERKRQRSFFLFG 299

446 LALIVQFDTEGIRSFRTFFRLPKMMWQGLGSTLTSGDLVLFALYMFVI 495

300 LALILQLDIEGIRSFFRAFFRVPKMMWQGLGSSLSXADLM LFAFYMFII 349

496 SPNNLRKGLINHLISDPTGATMIKTYLKV 524

350 APNDMRRGLIRHLLSDPTGATLIRTYLTF 378

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## FIG. 17A

*Adonis palaestina* Ipil

1	attcatcttc	agcagcgctg	tcgtactctt	tctatatctt	cttccatcac
51	taacagtagt	cgccgacggt	tgaatcggct	attcgccctca	acgtcaacta
101	tgggtgaagt	cactgatgct	ggaatggatg	ctgttcagaa	gcgggtcatg
151	ttcgacgacg	aatgtatctt	ggtggatgag	aatgacaagg	tcgtcgggca
201	tgattccaaa	tacaactgtc	atttgatgga	aaagatagag	gcagaaaatt
251	tgcttcacag	agccttcagt	gttttcttgt	tcaactcaaa	atatgaattg
301	cttcttcagc	aacgatccgc	cacaaaggta	acattcccgc	tcgtatggac
351	aaacacatgt	tgagtcctc	ctctctttcg	tgattccgag	ctcatagaag
401	aaaattatct	cggtgtacga	aacgctgcac	aaagaaagct	tttagacgag
451	ctaggcattc	cagctgaaga	tgtcccagtt	gatgaattta	ctcctcttgg
501	tcgcattctt	tacaaagctc	catctgacgg	caaattggga	gagcacgaat
551	tggactatct	cctattttatt	gtccgagatg	tgaaatacga	tccaaaccca
601	gatgaagttg	ctgatgctaa	gtatgttaat	cgcgaggagt	tgagagagat
651	actgagaaaa	gctgatgctg	gtgaagaggg	actcaagttg	tctccttggg
701	ttagattggg	tggtgataac	tttttggtca	agtgggtggg	tcatgtagag
751	cagggtacga	ttaaggaagt	tgctgacatg	aaaactatcc	acaagttgac
801	ttaagaggac	ttctctcctc	tggttctacta	tttggttttt	gctacaataa
851	gtgggtggg	ataagcagtt	tttctgtttt	ctttaattta	tggcttttga
901	atttgcctcg	atgttgaact	tgtaacatat	ttagacaaat	atgagacctt
951	gtaagttgaa	tttgaggctg	aatttatatt	tttggaaca	taataatggt
1001	aa				

P0560 "SEE P0200"

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## FIG. 17B

*Adonis palaestina Ipi2*

1	ttttaaaagct	ctttcgctcc	accaccatca	aagccagcca	aattttctctg
51	tacaaaagtt	aaaaacaccg	ctttgggctt	tggcccctcc	atatcggaat
101	ccttgtttac	gatacgcatc	taaaccagta	attctcggtt	ttaatttggt
151	tcctaaatta	ggcccctttc	cggaatcccg	agaattatgt	cgtcgatcag
201	gattaatcct	ttatatagta	tcttctccac	caccactaaa	acattatcag
251	cttcgtgttc	ttctcccgt	gttcattctc	agcagcgttg	tcgtactctt
301	tctatttctt	cttccatcac	taacagtcct	cgccgagggg	tgaatcggct
351	gttcgcctca	acgtcgacta	tgggtgaagt	cgctgatgct	ggtatggatg
401	ccgtccagaa	gcggcttatg	ttcgacgatg	aatgtatgtt	ggtggatgag
451	aatgacaagg	tcgtcggaca	tgattccaaa	tacaactgtc	atttgaatgga
501	aaagatagag	gcagaaaact	tgcttcacag	agccttcagt	gttttcttat
551	tcaactcaaa	atacgagtgt	cttcttcagc	aacgatctgc	aacgaaggta
601	acattcccgc	tcgtatggac	aaacacctgt	tgcagccatc	ccctcttccg
651	tgattccgaa	ctcatagaag	aaaattttct	cggggtacga	aacgctgcac
701	aaaggaagct	tttagacgag	ctaggcattc	cagctgaaga	cgtaccagtt
751	gatgaattca	ctcctcttgg	tcgcattctt	tacaaagctc	catctgacgg
801	aaaatgggga	gagcacgaac	tggactatct	tctgtttatt	gtccgagatg
851	tgaaatacga	tccaaaccca	gatgaagttg	ctgacgctaa	gtacgttaat
901	cgcgaggagt	tgaaagagat	actgagaaaa	gctgatgcag	gtgaagaggg
951	aataaaagttg	tctccttggt	ttagattggt	tgtggataac	tttttgttca
1001	agtgggtggga	tcatgtagag	gaggggaaga	ttaaggacgt	cgccgacatg
1051	aaaactatcc	acaagttgac	ttaagagaaa	gtctcttaag	ttctactatt
1101	tggtttttgc	ttcaataagt	ggatggatgat	gagcagtttt	tatgcttcct
1151	ttaatttttg	cttttcaatt	tgctttatgt	ggtgaacttg	taacatatatt
1201	agtcaaatat	gagaccttgt	gagttgaatt	tgagggtata	tttatagttt
1251	tggaacata	aaaaaaaaa			

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

FIG. 17B "SEE FIG. 17A"



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## FIG. 18A

*Haematococcus pluvialis* Ipil

1	ctcggtagct	ggccacaatc	gctatttgga	acctggcccg	gcggcagtcc
51	gatgccgcga	tgcttcgttc	gttgctcaga	ggcctcacgc	atatcccccg
101	cgtgaactcc	gccagcagc	ccagctgtgc	acacgcgcga	ctccagttta
151	agctcaggag	catgcagatg	acgctcatgc	agcccagcat	ctcagccaat
201	ctgtcgcgcg	ccgaggaccg	cacagaccac	atgaggggtg	caagcacctg
251	ggcaggcggg	cagtcgcagg	atgagctgat	gctgaaggac	gagtgcattc
301	tggtggatgt	tgaggacaac	atcacaggcc	atgccagcaa	gctggagtgt
351	cacaagttcc	taccacatca	gcctgcaggc	ctgctgcacc	gggccttctc
401	tgtgttcctg	tttgacgatc	aggggcgact	gctgctgcaa	cagcgtgcac
451	gctcaaaaat	caccttccca	agtgtgtgga	cgaacacctg	ctgcagccac
501	cctttacatg	ggcagacccc	agatgaggtg	gaccaactaa	gccaggtggc
551	cgacggaaca	gtacctggcg	caaaggctgc	tgccatccgc	aagttaggagc
601	acgagctggg	gataccagcg	caccagctgc	cggcaagcgc	gtttcgcttc
651	ctcacgcgtt	tgcaactactg	tgccgcggac	gtgcagccag	ctgcgacaca
701	atcagcgctc	tggggcgagc	acgaaatgga	ctacatcttg	ttcatccggg
751	ccaacgtcac	cttggcgccc	aaccctgacg	aggtggacga	agtcaggtac
801	gtgacgcaag	aggagctgcg	gcagatgatg	cagccggaca	acgggctgca
851	atggtcgccg	tggtttcgca	tcacgcggc	gcgcttcctt	gagcgttggt
901	gggctgacct	ggacgcggcc	ctaaacactg	acaaacacga	ggattgggga
951	acggtgcatc	acatcaacga	agcgtgaaag	cagaagctgc	aggatgtgaa
1001	gacacgtcat	gggggtggaat	tgcgtacttg	gcagcttcgt	atctcctttt
1051	tctgagactg	aacctgcagt	caggtcccac	aaggtcaggt	aaaatggctc
1101	gataaaatgt	accgtcactt	tttgtcgcgt	atactgaact	ccaagaggtc
1151	aaaaaaaaaa	aaaaa			

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## FIG. 18B

*Haematococcus pluvialis* Ipi2

1	tggaacctgg	cccggcggca	gtccgatgcc	gcgatgcttc	gttcgttgct
51	cagaggcctc	acgcataatcc	cgcgcgtagaa	ctccgcccag	cagcccagct
101	gtgcacacgc	gcgactccag	tttaagctca	ggagcatgca	gctgcttgcc
151	gaggaccgca	cagaccacat	gaggggtgca	agcacctggg	caggcgggca
201	gtcgcaggat	gagctgatgc	tgaaggacga	gtgcatctta	gtggatgctg
251	acgacaacat	cacaggccat	gccagcaagc	tggagtggca	caaattccta
301	ccacatcagc	ctgcaggcct	gctgcaccgg	gccttctctg	tggtcctggt
351	tgacgaccag	gggcgactgc	tgctgcaaca	gcgtgcacgc	tcaaaaatca
401	ccttcccaag	tgtgtggacg	aacacctgct	gcagccaccc	tctacatggg
451	cagaccccag	atgaggtgga	ccaactaagc	caggtggccg	acggcacagt
501	acctggcgca	aaagctgctg	ccatccgcaa	gttgagcac	gagctgggga
551	taccagcgca	ccagctgccg	gcaagcgct	ttcgcttcct	cacgcgtttg
601	cactactgtg	ccgcggacgt	gcagccggct	gcgacacaat	cagcgctctg
651	gggcgagcac	gagatggact	acatcttatt	catccggggc	aacgtcacct
701	tggcgcccaa	ccctgacgag	gtggacgaag	tcaggtacgt	gacgcaagag
751	gagctgcggc	agatgatgca	gccggacaac	gggttgcaat	ggtcgccgtg
801	gtttcgcatc	atcgccgcgc	gcttccttga	gcgttggtgg	gctgacctgg
851	acgcggccct	aaacactgac	aaacacgagg	attggggaac	ggtgcatcac
901	atcaacgaag	cgtgaaggca	gaagctgcag	gatgtgaaga	cacgtcatgg
951	ggtggaattg	cgtacttggc	agcttcgtat	ctcctttttc	tgagactgaa
1001	cctgcagagc	tagagtcaat	ggtgcatcat	attcatcgtc	tctcttttgt
1051	tttagactaa	tctgtagcta	gagtcactga	tgaatccttt	acaactttca
1101	aaaaaaaa				

## FIG. 19A

*Lactuca sativa Ipi1*

1	tgccaaaatg	ttgaaatttc	ccccttttaa	aaccattgct	accatgatct
51	cttctccata	ttcttccttc	ttgctgcctc	ggaaatcttc	tttccctcca
101	atgccgtctc	tgcagccgc	tagtgttttc	ctccaccctc	tttcgtctgc
151	cgctatgggc	gattccagca	tggatgctgt	ccagcgacgt	ctcatgttcg
201	atgacgaatg	cattttggtg	gatgagaatg	acaaagtggg	tggccatgat
251	actaaataca	attgtcattt	gatggagaag	attgaaaagg	gaaatatgct
301	acacagagca	ttcagtgtgt	tcttggttcaa	ctcgaaatat	gaattactcc
351	ttcagcaacg	ttctgcaacc	aagggtgactt	tccctttggg	atggacaaac
401	acgtgttgca	gccatccact	atacagggag	agtgaactta	ttgacgaaaa
451	cgcccttggg	gtgaggaatg	ctgcacagag	gaagctcctg	gatgaactcg
501	gcacccctgg	agcagatgtt	ccggttgatg	agttcactcc	attgggtcgc
551	attctataca	aggccgcac	ggatggaaaag	tggggagaaac	atgaacttga
601	ttacctgctg	tttatggtac	gtgatgttgg	tttggatccg	aaccagatg
651	aagtgaaga	tgtaaaatat	gtgaaccggg	aagagctgaa	ggaattggtg
701	aggaaggcgg	atgctggtga	agaggtgtg	aagctgtccc	cgtggttcaa
751	attgattgtc	gataatttct	tgtttcagtg	gtgggatcga	ctccataagg
801	gaaccctaac	cgaagctatt	gatatgaaaa	caatccacaa	actcacataa
851	aaacactaca	ctagtaggag	agaggattat	atgagatatt	tgttatatgt
901	gaaattgaaa	ttcagatgaa	tgcttgattt	tatttctatt	tggacaaact
951	tcaacttctt	tttgtctact	tatcagaaaa	aaaaa	

## FIG. 19B

*Lactuca sativa Ipi2*

1	tattcgcttc	aaaatctctt	ccattaactg	ctcaaattctc	caccttcgcc
51	ggtcttaatc	tccgccggcg	cactttcacc	accataaccg	ccgccatggg
101	tgacgattcc	ggcatggacg	ctgtccagag	acgtctcatg	tttgatgatg
151	aatgcatttt	ggttgatgaa	aatgacaatg	ttcttgggca	tgaataccaaa
201	tacaattgtc	acttgatgga	gaagattgag	aaagataatt	tgcttcatag
251	agcattcagt	gtatttttat	tcaattcaaa	atacgaatta	ctccttcagc
301	aaaggtcaga	aaccaagggtg	acatttcctt	tggtatggac	aaacacctgt
351	tgcagccatc	cactatacag	agaatcggag	ttaattccccg	aaaatgccct
401	tggggtcaga	aatgctgcac	agaggaagct	tctagatgaa	ctcggtatcc
451	ctgctgaaga	tgttccagtt	gatgagttca	caactttagg	tgcgatgttg
501	tacaaggctc	catctgatgg	aaaatggggg	gaacatgaag	ttgattacct
551	actcttcctc	gtgctgacg	ttgccgtgaa	cccaaaccct	gatgaggtgg
601	cggacattag	atacgtgaac	caagaagagt	taaaagagtt	actaaggaag
651	gcggatgcgg	gtgaggaggg	tttgaaattg	tccccatggt	ttaggctagt
701	ggtggacaac	ttcttggttca	aatggtggga	tcatgtccaa	aaggggacac
751	tcaatgaagc	aattgacatg	aaaaccattc	ataagttgat	atgaaaaatg
801	gttaattatt	atggtggtgg	tttgagacta	ataattttgtg	tgttcaagtc
851	tccgtccttc	tttttttaac	gttttttttt	tttcttttat	tgggagtgtt
901	tattgtgtac	ttgtaacgta	ggccctttgg	ttacgcttta	agagtttaat
951	aaagaaccac	cgtaatttta	aaaaaaaaaa	aaaaaaaaa	

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## FIG. 20

*Chlamydomonas reinhardtii* Ipi1

(Note: the isomerase cDNA probably ends at ca. base 1103; the second half of the cDNA is similar to extensin and other hydroxyproline-rich structural proteins)

1	ggcacgagct	cgagtttgtt	ttaccatgac	atcggaatt	tggaagcttg
51	aactacctca	attactcaag	taactcgcg	caacacattt	cgcgcgccat
101	cgctgttttc	tctgctccag	ctaccgagca	gcattgcttt	agatcgcttt
151	gatgtcataa	actcccactt	atatgagatc	cagtttcac	gagcccaagc
201	ccagagcgca	acctgtctta	agccgcgga	gggctccat	gcgcctcgcg
251	caaagccgtg	ctctcggtgc	gcgtgtcagc	tccgccctgt	ggccgggagc
301	aggactttca	caggctcaaa	gcgttgccgt	gcgaatggcg	agttcgctaa
351	cctgggaagg	cacgggcctg	agccaggatg	acttcatgca	gcgggacgag
401	tgcttggtgg	tggacgagca	ggaccggctg	ctaggcaccg	ccaacaagta
451	cgactgccac	cgcttcgagg	cgcccaagg	ccagccctgc	ggccgcctgc
501	accgcgcctt	ctccgtgttc	ctgttcagcc	ccgacggccg	actgctgctg
551	cagcagcgcg	cagccagcaa	ggtgacgttc	ccgggtgtgt	ggaccaacac
601	ctgctgctcg	caccgcgtgg	cgggccaggc	gccggacgag	gtggacctgc
651	cgggcgcggt	agcctcgggc	caggtgccgg	gcatcaaggc	ggcggcggtg
701	cgcaagctgc	agcacgagct	gggataaccg	ccggagcagg	ttcccgccctc
751	ctccttctcc	ttcctcacgc	gtctgcacta	ctgcgccgcc	gacaccgcca
801	cgcacggccc	ggcggcggag	tggggcgagc	acgaggtgga	ctacgtgctg
851	ttcgtgcggc	cgcagcagcc	cgtcagcctg	cagcccaacc	cagacgaggt
901	ggacgccacg	cgctacgtga	cgctgccgga	gcttcagtcc	atgatggcgg
951	accccgccct	cagctggagc	ccctggttcc	gcatcctggc	cacacagccc
1001	gccttcctgc	ccgcctgggtg	gggacgacctg	aagcggcgct	ggcgcccggg
1051	cggcagccga	ctgtaggact	ggggcaccat	ccaccgcgtc	atgtgaagaa
1101	aaaggggaag	cagggggcggg	agcgggggat	gaatgggaat	gtgaatgcga
1151	ttgtgatgag	gcgtgggatg	aggtctgaag	acagggggaa	aatcgggggg
1201	cgggcgtag	cggtgtgtga	cgtagcgcac	aaagccggga	ggcggaaccgc
1251	gcgatgggta	catgtgtgtg	cggagggtcg	gtgggtcggt	cggttgcgcg
1301	gcatagcgtg	ttgtgtgtgt	gcggctgcgc	gggtatgtgg	gcacccgggc
1351	acggaggaga	aggcacacgc	aggtggcgcg	gaggtgtgtc	aggggccatg
1401	ggcgggccctc	actcctggtc	gtgcccagtg	gtctcggtgg	cagagtggca
1451	ggggctgcac	ccatatgagc	ggcgactgc	cgcgctgggc	taagtcctta
1501	tcacttggtg	aggtggggcg	aggtggctgt	ggcgggcggg	cgagtgga
1551	gaaggacacg	gtgtgtgagc	ggtggagctc	tggccgtgcc	ggccgtgagg
1601	ggcgatagc	gatatgacgt	tgtgcttggc	cgctgtaatg	cgggagaatg
1651	tgcaggccgc	gagaagcggg	cggtggcagg	aggccgcagg	ctgcagcacc
1701	cggtggggag	gtgccgcctg	caggcgcggc	gccgggcggg	cctgagtaat
1751	ggcgccctga	gtagtggcgg	ccacaggagg	cgcaggaggc	agcagcagga
1801	ggacgagctg	gagggacccg	ttggcaaccc	aaggttgcgc	gtgtaacata
1851	gtggccatac	aaaaaaaaaa	aaaa		

## FIG. 21A

*Tagetes erecta* Ipil

1	ccaaaaacaa	ctcaaattctc	ctccgctcgct	cttactccgc	catgggtgac
51	gactccggca	tggatgctgt	tcagcgacgt	ctcatgtttg	acgatgaatg
101	catttttggtg	gatgagtgtg	acaatgtggg	gggacatgat	accaaataca
151	attgtcactt	gatggagaag	attgaaacag	gtaaaatgct	gcacagagca
201	ttcagcgttt	ttctattcaa	ttcaaaatac	gagttacttc	ttcagcaacg
251	gtctgcaacc	aaggtgacat	ttcctttagt	atggaccaac	acctgttgca
301	gccatccact	ctacagagaa	tccgagcttg	ttcccgaata	cgcccttgga
351	gtaagaaatg	ctgcacagag	gaagctgttg	gatgaactcg	gtatccctgc
401	tgaagatgtt	cccgttgatc	agtttactcc	tttaggtcgc	atgctctaca
451	aggctccatc	tgatggaaag	tggggagaac	atgaacttga	ctacctactt
501	ttcatagtga	gagacgttgc	tgtaaacccg	aaccagatg	aagtggcgga
551	tatcaaata	gtganccang	aagagttaaa	ggagctgcta	aggaaagcag
601	atgcggggga	ggagggtttg	aagctgtctc	catggttcag	gttagtggtt
651	gataacttct	tgttcaagtg	gtgggatcat	gtgcaaaagg	gtacactcac
701	tgaagcaatt	gatatgaaaa	ccatacacaa	gctgatatag	aaacacaccc
751	tcaaccgaaa	agttcaagcc	taataattcg	ggttgggtcg	ggtctaccat
801	caattgtttt	tttcttttaa	gaagttttta	tctctatttg	agcatgttga
851	ttcttgtctt	ttgtgtgtaa	gattttgggt	ttcgtttcag	ttgtaataat
901	gaaccattga	tggtttgcaa	tttcaagttc	ctatcgacat	gtagtgatct
951	aaaaaa				

## FIG. 21B

*Oryza sativa* Ipil

1	cctccctttg	cctcgcgcag	aggcggccgc	gccttctccg	ccgcgaggat
51	ggccggcgcc	gccgcccgcg	tggaggacgc	cgggatggac	gaggtccaga
101	agcggctcat	gttcgacgac	gaatgcattt	tgggtggatga	acaagacaat
151	gttggtggcc	atgaatcaaa	atataactgc	catctgatgg	aaaaaatcga
201	atctgaaaat	ctacttcata	gggctttcag	tgtattcctg	ttcaactcaa
251	aataatgaact	cctactccag	caacgatctg	caacaaagg	tacatttcct
301	ctagtgttga	ccaacacttg	ctgcagccat	cctctgtacc	gtgagtctga
351	gcttatacag	gaaaactacc	ttggtgttag	aaatgctgct	cagaggaagc
401	tcttggtatga	gctgggcatc	ccagctgaag	atgtgccagt	tgaccaattc
451	accctcttg	gtcggatgct	ttacaaggcc	ccatctgatg	gaaaatgggg
501	tgaacacgag	cttgactacc	tgtgtttcat	cgtccgcgac	gtgaaggtag
551	tcccgaaccc	ggacgaagtg	gccgatgtga	aatacgtgag	ccgtgagcag
601	ctgaaggagc	tcatccgcaa	agcggacgcc	ggagaggaag	gcctgaagct
651	gtctccctgg	ttccggctgg	ttgttgacaa	cttccctcatg	ggctggtggg
701	atcacgtcga	gaaaggcacc	ctcaacgagg	ccgtggacat	ggagaccatc
751	cacaagctga	agtaaggact	gcgatgttgt	ggctggaaag	aatgatcctg
801	aagactctgt	tcttgtgctg	ctgcatatta	ctcttaccag	ggaagttgca
851	gaagtcagaa	gaagcttttg	tatgtttctg	ggtttgagac	ttggaagtgt
901	tgggctctgc	tgactgagag	attcccttat	agagtgtcta	tgtaatttta
951	gcaaacttct	atattataca	tgattagtta	attgttcggg	gtctgaataa
1001	agaacaatag	catgttccat	gtttatttgc	t	

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ClustalW 1.7 Multiple Sequence Alignment of Plant and Green Algal Isopentenyl Pyrophosphate Isomerases (IPI)  
 These amino acid sequences were predicted by cDNAs that were isolated and identified by color complementation in *E. coli*

	1	15	16	30	31	45	46	60	61	75	76	90
1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
27	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
75	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
27	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
90	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
33	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
80	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
74	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
86	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
84	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
111	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
107	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
155	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
107	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
170	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
109	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
113	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
160	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
109	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
162	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
174	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
174	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

FIG. 22A

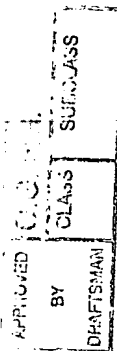


FIG. 22B "SEE FIG. 22A"

	181	195	196	210	211	225	226	240	241	255	256	270	
1 <i>T. erecta</i> 1	AQRKLLDELGIPAED	VPVQFTPLGRMLY	--KAPSDG----	KWG	EHELDYLLFIVRD--	VAVNPNPDEVADIKY	VSHEELKELLRKADA	188					
2 <i>L. sativa</i> 1	AQRKLLDELGIPGAD	VPVDEFTPLGRILY	--KAASDG----	KWG	EHELDYLLFIVRD--	VGLDPNPDEVKDVKY	VNREELKELVRKADA	236					
3 <i>L. sativa</i> 2	AQRKLLDELGIPAED	VPVDEFTPLGRMLY	--KAPSDG----	KWG	EHEVDYLLFIVRD--	VAVNPNPDEVADIRY	VNQEELKELLRKADA	188					
4 <i>A. palaestina</i> 2	AQRKLLDELGIPAED	VPVDEFTPLGRILY	--KAPSDG----	KWG	EHELDYLLFIVRD--	VKYDPNPDEVADAKY	VNREELKEILRKADA	251					
5 <i>A. palaestina</i> 1	AQRKLLDELGIPAED	VPVDEFTPLGRILY	--KAPSDG----	KWG	EHELDYLLFIVRD--	VKYDPNPDEVADAKY	VNREELREILRKADA	190					
6 <i>O. sativa</i> 1	AQRKLLDELGIPAED	VPVQFTPLGRMLY	--KAPSDG----	KWG	EHELDYLLFIVRD--	VKVVPNPDEVADVKY	VSREQLKELIRKADA	194					
7 <i>A. thaliana</i> 1	AQRKLLDELGIVAED	VPVDEFTPLGRMLY	--KAPSDG----	KWG	EHELDYLLFIVRD--	VKVQPNPDEVAEIKY	VSREELKELVKKADA	241					
8 <i>A. thaliana</i> 2	AQRKLFDELGIVAED	VPVDEFTPLGRMLY	--KAPSDG----	KWG	EHEVDYLLFIVRD--	VKLQPNPDEVAEIKY	VSREELKELVKKADA	190					
9 <i>H. pluvialis</i> 1	AIRKLEHELGIPIAHQ	LPASAFRLTRLHYC	AADVQPAATQSALWG	EHEMDYILFIRAN--	VTLAPHPDEVDEVRY	VTQELRQMMQP----		247					
10 <i>H. pluvialis</i> 2	AIRKLEHELGIPIAHQ	LPASAFRLTRLHYC	AADVQPAATQSALWG	EHEMDYILFIRAN--	VTLAPNPDEVDEVRY	VTQELRQMMQP----		259					
11 <i>C. reinhardtii</i> 1	AVRKLQHELGIPIPEQ	VPASSFSLTRLHYC	AADTATHG--PAAEWG	EHEVDYVLFVRPQQP	VSLQPNPDEVADTRY	VTLPQLQSMMA----		259					

	271	285	286	300	301	315	316						
1 <i>T. erecta</i> 1	GEEGLKLSMPFRLVV	DN--FLFKMWDHVQK	GTL----	TEAIDMKTI	HKLI--	232	<i>Tagetes erecta (marigold)</i>						
2 <i>L. sativa</i> 1	GEEGVKLSMPFKLIV	DN--FLFKMWDRLHK	GTL----	TEAIDMKTI	HKLT--	280	<i>Lactuca sativa (romaine lettuce)</i>						
3 <i>L. sativa</i> 2	GEEGLKLSMPFRLVV	DN--FLFKMWDHVQK	GTL----	NEAIDMKTI	H-----	229	<i>Lactuca sativa (romaine lettuce)</i>						
4 <i>A. palaestina</i> 2	GEEGIKLSMPFRLVV	DN--FLFKMWDHVEE	GKI----	KDVADMKTI	HKLT--	295	<i>Adonis palaestina (pheasant's eye)</i>						
5 <i>A. palaestina</i> 1	GEEGLKLSMPFRLVV	DN--FLFKMWDHVEQ	GTL----	KEVADMKTI	HKLT--	234	<i>Adonis palaestina (pheasant's eye)</i>						
6 <i>O. sativa</i> 1	GEEGLKLSMPFRLVV	DN--FLFKMWDHVEK	GTL----	NEAVDMETI	HKLK--	238	<i>Oryza sativa (rice)</i>						
7 <i>A. thaliana</i> 1	GEEGLKLSMPFRLVV	DN--FLFKMWDHVEK	GTL----	VEAIDMKTI	HKL----	284	<i>Arabidopsis thaliana</i>						
8 <i>A. thaliana</i> 2	GDEAVKLSMPFRLVV	DN--FLFKMWDHVEK	GTL----	TEAIDMKTI	HKL----	233	<i>Arabidopsis thaliana</i>						
9 <i>H. pluvialis</i> 1	-DHGLQWSPWFRILIA	AR--FLERWADLDA	ALN--	TDKHEDWGTIV	HHINEA	293	<i>Haematococcus pluvialis</i>						
10 <i>H. pluvialis</i> 2	-DHGLQWSPWFRILIA	AR--FLERWADLDA	ALN--	TDKHEDWGTIV	HHINEA	305	<i>Haematococcus pluvialis</i>						
11 <i>C. reinhardtii</i> 1	-DPGLSWSPWFRILA	TOPAFLPAMWGD LKR	RWRPGGSR LSWGTI	HRVM--		307	<i>Chlamydomonas reinhardtii</i>						

FIG. 22B

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APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

FIG. 23

FIG. 23A
FIG. 23B
FIG. 23C
FIG. 23D

FIG. 23

FIG. 24 A
FIG. 24B

FIG. 24

FIG. 25A
FIG. 25B
FIG. 25C

FIG. 25

FIG. 28A
FIG. 28B

FIG. 28

FIG. 26A
FIG. 26B

FIG. 26



## FIG. 23A

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Comparison using GAP program of the Genetics Computer Group

Gap Weight: 50

Average match: 10.000

Length Weight: 3

Average Mismatch: 0.000

Quality: 17392

Length: 1904

Ratio: 9.411

Gaps: 3

Percent Similarity: 95.331

Percent Identity: 95.331

Match display thresholds for the alignment(s):

| = IDENTITY : = 5 . = 1

*Adonis palaestina*  $\epsilon$ -cyclase #3 x *Adonis palaestina*  $\epsilon$ -cyclase #5

```

1 gagagaaaaagagtgttatattaatgttactgtcgcattcttgcaacac. 49
  |||
1 .....aaaggagtgttctattaatgttactgtcgcattcttgcaacact 44
50 .atattcagactccattttcttggtttctcttcaaaacaacaaactaatg 98
  |||
45 tatattcaaactccattttcttcttttctcttcaaaacaacaaactaatg 94
99 tga.cggagtatctagctatggaactacttggtgttcgcaacctcatctc 147
  |||
95 tgagcagagtatctggctatggaactacttggtgttcgcaacctcatctc 144
148 ttcttgccctgtctggacttttggaacaagaaaccttagtagttcaaaac 197
  |||
145 ttcttgccctgtgtggacttttggaacaagaaaccttagtagttcaaaac 194
198 tagcttataacatacatcgatatggttcttcttgtagagtagattttcaa 247
  |||
195 tagcttataacatacatcgatatggttcttcttgtagagtagattttcaa 244
248 gtgagggctgatggtggaagcgggagtagaacttctggtgcttataaaga 297
  |||
245 gtgagagctgatggtggaagcgggagtagaagttctggtgcttataaaga 294
298 gggttttgtggacgaggaggattttatcaaagctggtggttctgagcttt 347
  |||
295 gggttttgtggatgaagaggattttatcaaagctggtggttctgagcttt 344
348 tgtttgtccaaatgcagcaaaacaaagtctatggagaaacaggccaagctc 397
  |||
345 tgtttgtccaaatgcagcaaaacaaagtctatggagaaacaggccaagctc 394

```

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## FIG. 23B

398 gccgataagttgccaccaataccttttcggagaatctgtgatggacttgggt 447  
395 gccgataagttgccaccaataccttttggagaatccgtgatggacttgggt 444  
448 tgtaataggttgtggacctgctggctctttcactggctgcagaagctgcta 497  
445 tgtaataggttgtggacctgctggctctttcactggctgcagaagctgcta 494  
498 agctaggcttgaaagttggccttattggctcctgatcttccttttacaat 547  
495 agctagggttgaaagttggccttattggctcctgatcttccttttacaat 544  
548 aattatggtgtgtgggaagacgagttcaaagatcttggacttgaacgttg 597  
545 aattatggtgtgtgggaagacgagttcaaagatcttggacttgaacgttg 594  
598 tatcgagcatgcttggaggacaccatcgtatatcttgacaatgatgctc 647  
595 tatcgagcatgcttggaggacaccatcgtatatcttgataatgatgctc 644  
648 ctgtccttattggtcgtgcataatggacgagttagccggcatttgctgcat 697  
645 ctgtccttattggtcgtgcataatggacgagttagtcgacatttgctacat 694  
698 gaagagttgctgaaaaggtgtgtcgagtcaggtgtatcatatctgaattc 747  
695 gaggagttgctgaaaaggtgtgtggagtcaggtgtatcatatctggattc 744  
748 taaagtggaaaggatcactgaagctggtgatggccatagtccttgtagttt 797  
745 taaagtggaaaggatcactgaagctggtgatggccatagccttgtagttt 794  
798 gtgaaaacgacatctttatcccttgaggcttgctactgttgcatctgga 847  
795 gtgaaaatgagatctttatcccttgaggcttgctactgttgcatctgga 844  
848 gcagcttcagggaacttttggagtatgaagtaggtggccctcgtgtttg 897  
845 gcagcttcagggaacttttggagtatgaagtaggtggccctcgtgtttg 894  
898 tgtccaaactgcttatggtgtggaggttgaggtggagaacaatccatacg 947  
895 tgtccaaaccgcttatggggtggaggttgaggtggagaacaatccatacg 944

## FIG. 23C

948 atcccaacttaatggtatttattggactacagagactatatgcaacagaaa 997  
 945 atcccaacttaatggtatttcatggactacagagactatatgcaacagaaa 994  
 998 ttacagtgctcggagaagaatatccaacatttctctatgtcatgcccatt 1047  
 995 ttacagtgctcggagaagaatatccaacatttctctatgtcatgcccatt 1044  
 1048 gtcgccaacaagacttttttttgaggaaacctgtttggcctcaaaagatg 1097  
 1045 gtcgccaacaagacttttttttgaggaaacctgtttggcctcaaaagatg 1094  
 1098 ccatgcctttcgatctactgaagagaaaactaatgtcacgattgaagact 1147  
 1095 ccatgccatttcgatctactgaagagaaaactgatgtcacgattgaagact 1144  
 1148 ctgggtatccaagttacaaaatttatgaagaggaatggcttatattcc 1197  
 1145 ctgggtatccaagttacaaaagtttatgaagaggaatggctatatattcc 1194  
 1198 tgttggtgggttctttaccaaacacagagcaaaagaacctagcatttggtg 1247  
 1195 tgttggtgggttctttaccaaacacagagcaaaagaacctagcatttggtg 1244  
 1248 ctgcagcaagcatggtgcatccagcaacaggctattcggttgtagcatca 1297  
 1245 ctgcagcaagcatggtgcatccagcaacaggctattcggttgtagcggtca 1294  
 1298 ctatcagaagctccaaaatatgcttctgtaattgcaaagattttgaagca 1347  
 1295 ctgtcagaagctccaaaatatgcttctgtaattgcaaagattttgaagca 1344  
 1348 agataactctgcatatgtggtttctggacaaagcagtgtagtaaacattt 1397  
 1345 agataactctgcatatgtggtttctggacaaagcagtgtagtaaacattt 1394  
 1398 caatgcaagcatggagcagctctttggccaaaggagcgaaaacgtcaaaga 1447  
 1395 caatgcaagcatggagcagctctttggccaaaggagcgaaaacgtcaaaga 1444  
 1448 gcattctttcttttcgggttagagcttattgtgcagctagatattgaagc 1497  
 1445 gcattctttcttttcgggttagagcttattgtgcagctagatattgaagc 1494

APPROVED	002 H-24	CLASS	SUCCESS
BY			
DRAFTSMAN			

1. *Chlorophyll a* (Chl *a*)  
 2. *Chlorophyll b* (Chl *b*)  
 3. *Chlorophyll c* (Chl *c*)  
 4. *Chlorophyll d* (Chl *d*)  
 5. *Chlorophyll e* (Chl *e*)  
 6. *Chlorophyll f* (Chl *f*)  
 7. *Chlorophyll g* (Chl *g*)  
 8. *Chlorophyll h* (Chl *h*)  
 9. *Chlorophyll i* (Chl *i*)  
 10. *Chlorophyll j* (Chl *j*)  
 11. *Chlorophyll k* (Chl *k*)  
 12. *Chlorophyll l* (Chl *l*)  
 13. *Chlorophyll m* (Chl *m*)  
 14. *Chlorophyll n* (Chl *n*)  
 15. *Chlorophyll o* (Chl *o*)  
 16. *Chlorophyll p* (Chl *p*)  
 17. *Chlorophyll q* (Chl *q*)  
 18. *Chlorophyll r* (Chl *r*)  
 19. *Chlorophyll s* (Chl *s*)  
 20. *Chlorophyll t* (Chl *t*)  
 21. *Chlorophyll u* (Chl *u*)  
 22. *Chlorophyll v* (Chl *v*)  
 23. *Chlorophyll w* (Chl *w*)  
 24. *Chlorophyll x* (Chl *x*)  
 25. *Chlorophyll y* (Chl *y*)  
 26. *Chlorophyll z* (Chl *z*)  
 27. *Chlorophyll aa* (Chl *aa*)  
 28. *Chlorophyll ab* (Chl *ab*)  
 29. *Chlorophyll ac* (Chl *ac*)  
 30. *Chlorophyll ad* (Chl *ad*)  
 31. *Chlorophyll ae* (Chl *ae*)  
 32. *Chlorophyll af* (Chl *af*)  
 33. *Chlorophyll ag* (Chl *ag*)  
 34. *Chlorophyll ah* (Chl *ah*)  
 35. *Chlorophyll ai* (Chl *ai*)  
 36. *Chlorophyll aj* (Chl *aj*)  
 37. *Chlorophyll ak* (Chl *ak*)  
 38. *Chlorophyll al* (Chl *al*)  
 39. *Chlorophyll am* (Chl *am*)  
 40. *Chlorophyll an* (Chl *an*)  
 41. *Chlorophyll ao* (Chl *ao*)  
 42. *Chlorophyll ap* (Chl *ap*)  
 43. *Chlorophyll aq* (Chl *aq*)  
 44. *Chlorophyll ar* (Chl *ar*)  
 45. *Chlorophyll as* (Chl *as*)  
 46. *Chlorophyll at* (Chl *at*)  
 47. *Chlorophyll au* (Chl *au*)  
 48. *Chlorophyll av* (Chl *av*)  
 49. *Chlorophyll aw* (Chl *aw*)  
 50. *Chlorophyll ax* (Chl *ax*)  
 51. *Chlorophyll ay* (Chl *ay*)  
 52. *Chlorophyll az* (Chl *az*)  
 53. *Chlorophyll ba* (Chl *ba*)  
 54. *Chlorophyll bb* (Chl *bb*)  
 55. *Chlorophyll bc* (Chl *bc*)  
 56. *Chlorophyll bd* (Chl *bd*)  
 57. *Chlorophyll be* (Chl *be*)  
 58. *Chlorophyll bf* (Chl *bf*)  
 59. *Chlorophyll bg* (Chl *bg*)  
 60. *Chlorophyll bh* (Chl *bh*)  
 61. *Chlorophyll bi* (Chl *bi*)  
 62. *Chlorophyll bj* (Chl *bj*)  
 63. *Chlorophyll bk* (Chl *bk*)  
 64. *Chlorophyll bl* (Chl *bl*)  
 65. *Chlorophyll bm* (Chl *bm*)  
 66. *Chlorophyll bn* (Chl *bn*)  
 67. *Chlorophyll bo* (Chl *bo*)  
 68. *Chlorophyll bp* (Chl *bp*)  
 69. *Chlorophyll bq* (Chl *bq*)  
 70. *Chlorophyll br* (Chl *br*)  
 71. *Chlorophyll bs* (Chl *bs*)  
 72. *Chlorophyll bt* (Chl *bt*)  
 73. *Chlorophyll bu* (Chl *bu*)  
 74. *Chlorophyll bv* (Chl *bv*)  
 75. *Chlorophyll bw* (Chl *bw*)  
 76. *Chlorophyll bx* (Chl *bx*)  
 77. *Chlorophyll by* (Chl *by*)  
 78. *Chlorophyll bz* (Chl *bz*)  
 79. *Chlorophyll ca* (Chl *ca*)  
 80. *Chlorophyll cb* (Chl *cb*)  
 81. *Chlorophyll cc* (Chl *cc*)  
 82. *Chlorophyll cd* (Chl *cd*)  
 83. *Chlorophyll ce* (Chl *ce*)  
 84. *Chlorophyll cf* (Chl *cf*)  
 85. *Chlorophyll cg* (Chl *cg*)  
 86. *Chlorophyll ch* (Chl *ch*)  
 87. *Chlorophyll ci* (Chl *ci*)  
 88. *Chlorophyll cj* (Chl *cj*)  
 89. *Chlorophyll ck* (Chl *ck*)  
 90. *Chlorophyll cl* (Chl *cl*)  
 91. *Chlorophyll cm* (Chl *cm*)  
 92. *Chlorophyll cn* (Chl *cn*)  
 93. *Chlorophyll co* (Chl *co*)  
 94. *Chlorophyll cp* (Chl *cp*)  
 95. *Chlorophyll cq* (Chl *cq*)  
 96. *Chlorophyll cr* (Chl *cr*)  
 97. *Chlorophyll cs* (Chl *cs*)  
 98. *Chlorophyll ct* (Chl *ct*)  
 99. *Chlorophyll cu* (Chl *cu*)  
 100. *Chlorophyll cv* (Chl *cv*)  
 101. *Chlorophyll cw* (Chl *cw*)  
 102. *Chlorophyll cx* (Chl *cx*)  
 103. *Chlorophyll cy* (Chl *cy*)  
 104. *Chlorophyll cz* (Chl *cz*)  
 105. *Chlorophyll da* (Chl *da*)  
 106. *Chlorophyll db* (Chl *db*)  
 107. *Chlorophyll dc* (Chl *dc*)  
 108. *Chlorophyll dd* (Chl *dd*)  
 109. *Chlorophyll de* (Chl *de*)  
 110. *Chlorophyll df* (Chl *df*)  
 111. *Chlorophyll dg* (Chl *dg*)  
 112. *Chlorophyll dh* (Chl *dh*)  
 113. *Chlorophyll di* (Chl *di*)  
 114. *Chlorophyll dj* (Chl *dj*)  
 115. *Chlorophyll dk* (Chl *dk*)  
 116. *Chlorophyll dl* (Chl *dl*)  
 117. *Chlorophyll dm* (Chl *dm*)  
 118. *Chlorophyll dn* (Chl *dn*)  
 119. *Chlorophyll do* (Chl *do*)  
 120. *Chlorophyll dp* (Chl *dp*)  
 121. *Chlorophyll dq* (Chl *dq*)  
 122. *Chlorophyll dr* (Chl *dr*)  
 123. *Chlorophyll ds* (Chl *ds*)  
 124. *Chlorophyll dt* (Chl *dt*)  
 125. *Chlorophyll du* (Chl *du*)  
 126. *Chlorophyll dv* (Chl *dv*)  
 127. *Chlorophyll dw* (Chl *dw*)  
 128. *Chlorophyll dx* (Chl *dx*)  
 129. *Chlorophyll dy* (Chl *dy*)  
 130. *Chlorophyll dz* (Chl *dz*)  
 131. *Chlorophyll ea* (Chl *ea*)  
 132. *Chlorophyll eb* (Chl *eb*)  
 133. *Chlorophyll ec* (Chl *ec*)  
 134. *Chlorophyll ed* (Chl *ed*)  
 135. *Chlorophyll ee* (Chl *ee*)  
 136. *Chlorophyll ef* (Chl *ef*)  
 1

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APPROVED	CLASS	SUBCLASS
BY		
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FIG. 23D

1498 aaccagaacg<sup>.</sup>ttc<sup>.</sup>tttagaac<sup>.</sup>ctt<sup>.</sup>cttccg<sup>.</sup>cttgccaact<sup>.</sup>tggatgtgg<sup>.</sup>t 1547  
 |||||  
 1495 aaccagaacattc<sup>.</sup>tttagaac<sup>.</sup>ctt<sup>.</sup>cttccg<sup>.</sup>cttgccaact<sup>.</sup>tggatgtgg<sup>.</sup>t 1544  
 |||||  
 1548 gggg<sup>.</sup>tttc<sup>.</sup>cttgggtcttcactatcatct<sup>.</sup>ttcgatctt<sup>.</sup>gtattg<sup>.</sup>ttttcc 1597  
 |||||  
 1545 gggg<sup>.</sup>tttc<sup>.</sup>cttgggtcttcactatcatct<sup>.</sup>ttcgatctcgtctt<sup>.</sup>gttttcc 1594  
 |||||  
 1598 atgtacatg<sup>.</sup>ttt<sup>.</sup>gttttgg<sup>.</sup>ccccgaacagcatgaggatgtcactt<sup>.</sup>gtgag 1647  
 |||||  
 1595 atgtacatg<sup>.</sup>ttt<sup>.</sup>gttttggcgccaaacagcatgaggatgtcactt<sup>.</sup>gtgag 1644  
 |||||  
 1648 acattt<sup>.</sup>gctt<sup>.</sup>tcagatcctt<sup>.</sup>ctggtgcagttat<sup>.</sup>ggttaa<sup>.</sup>agcttacctc<sup>.</sup>g 1697  
 |||||  
 1645 acattt<sup>.</sup>gctt<sup>.</sup>tcagatcctt<sup>.</sup>ctggtgcagttat<sup>.</sup>ggttaa<sup>.</sup>agagcttacctc<sup>.</sup>g 1694  
 |||||  
 1698 aaaggtaatc<sup>.</sup>...tg<sup>.</sup>ttttatgaaactatagtgtctcat<sup>.</sup>taaataaatga 1744  
 |||||  
 1695 aaaggtagtctcatctattattaaactctagtgttccaccaaataaatga 1744  
 |||||  
 1745 ggatccttcgtatatgtatatgatcatctctatgtatatcctatattct<sup>.</sup>a 1794  
 |||||  
 1745 ggatccttcgaatgtgtatatgatcatctctatgtatatcctgtactct<sup>.</sup>a 1794  
 |||||  
 1795 atctcataaagtaatcgaaaattcattgatagaaaaaaaaaaaaaaaaaa 1844  
 |||||  
 1795 atctcataaagtaa<sup>.</sup>atgccgggtttgata<sup>.</sup>ttgttgtgtcaaaccggccaa 1844  
 |||||  
 1845 aaaa..... 1848  
 1845 tgatataaagtaaatttattgatacaaaagtagtttttttttttaaaaaa 1894

FIG. 23D

FIG. 24A

```

Gap Weight:      12      Average Match:      2.912
Length Weight:   4       Average Mismatch:     -2.003
Quality:      2728      Length:           530
Ratio:      5,147      Gaps:              0
Percent Similarity: 99,623  Percent Identity:  99.057
Match display thresholds for the alignment(s):
| = IDENTITY      : = 2      . = 1

```

*Adonis palaestina*  $\epsilon$ -cyclase #3 x *Adonis palaestina*  $\epsilon$ -cyclase #5

1 MELLGVRNLISSCPVWTFGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGG 50  
1 MELLGVRNLISSCPVWTFGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGG 50

51 SGSRTSVAYKEGFVDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPP 100  
51 SGSRSSVAYKEGFVDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPP 100

101 IPFGESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWE 150  
101 IPFGESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWE 150

151 DEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKR 200  
151 DEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKR 200

201 CVESGVSYLNSKVERITEAGDGHSLVVCENDIFIPCLATVASGAASGKL 250  
201 CVESGVSYLDSKVERITEAGDGHSLVVCENEIFIPCLATVASGAASGKL 250

251 LEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFM DYRDYMQQKLQCSEE 300  
251 LEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFM DYRDYMQQKLQCSEE 300

301 EYPTFLYVMPMSPTRLFEEETCLASKDAMPFDLLKRKLMSRLKTLGIQVT 350  
301 EYPTFLYVMPMSPTRLFEEETCLASKDAMPFDLLKRKLMSRLKTLGIQVT 350

[illegible]

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APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

351 KIYEEESYIPVGGSLPNTQKNLAFGAAASMVHPATGYSVVRSLSEAPK 400  
 |:|||||||||||||||||||||||||||||||||||||||||||  
 351 KUYEEESYIPVGGSLPNTQKNLAFGAAASMVHPATGYSVVRSLSEAPK 400  
 401 YASVIAKILKQDNSAYVVSGQSSAVNISMQAWSSLWPKERKRQRAFFLFG 450  
 |||||||||||||||||||||||||||||||||||||||||||||  
 401 YASVIAKILKQDNSAYVVSGQSSAVNISMQAWSSLWPKERKRQRAFFLFG 450  
 451 LELIVQLDIEATRTRFFRTFFRLPTWMMWGFLGSSLSSFDLVLFMYMFVL 500  
 |||||||||||||||||||||||||||||||||||||||||||||  
 451 LELIVQLDIEATRTRFFRTFFRLPTWMMWGFLGSSLSSFDLVLFMYMFVL 500  
 501 APNSMRMSLVRHLLSDPSGAVMVKAYLER\* 530  
 |||||||||||||||||||||:|||||||  
 501 APNSMRMSLVRHLLSDPSGAVMVRAYLER\* 530

FIG. 24B

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## FIG. 25A

PotatoE :  
 ArabidopsisE : MEVGAIRNF-AAWAVSTFPSWS-CRRKFPVVKRYSYRNIREFGL-CSV--RAGGGSSGSESCVAVREDF--ADEEDFVKAGGSEILFVQMQQNKMDQSKLVKLPPI : 103  
 AdonisE1 : MELLGVRNL-----ISSCPVMT-FGTRNLSSSKLAYNTHRYGSSCRVDQVRADGGSGSRSSVAYKEGF--VDEEDF IKAGGSELLFVQMQQTKSMEKQAKLADKLPPI : 102  
 AdonisE2 : MELLGVRNL-----ISSCPVMT-FGTRNLSSSKLAYNTHRYGSSCRVDQVRADGGSGSRSSVAYKEGF--VDEEDF IKAGGSELLFVQMQQTKSMEKQAKLADKLPPI : 102  
 LettuceEE : MEVGAIRNFMTAHTMAVFTCPRTDCNIRHKFSLKQRRFTNLISA-SSSLRQIKCSAKSDR--CVVDKQGISVADEEDYVYKAGGSELLFVQMQQTKSMEKQAKLADKLPPI : 107  
 TomatoE : MEVGVQNV-GAMAVLTRPRLN-----RWSGELCQKESIFLAY-EQY--ESKNSSSGSDSCVDKEDF--ADEEDY IKAGGSQLFVQMQQKMDQSKLSDELQPI : 100  
 MarigoldE : MSIRAG-HMTATMAAFTCPRPM-----TSIRYT-----KQIKCNAKSQ---LVKQEI--EEEEYVYKAGGSELLFVQMQQNKMDQSKLSDELQPI : 84  
 ArabidopsisB : -----MDTLTKTPNKLDFFIPQFHGFE--RLCSNPNYHSRVRGLGVKKRAIKIV-----SSWGSAAALDLVPETKKNLEDFEL : 72  
 AdonisB : -----MDTLRTHNKLELPTLHGFA--EKQLVSTSKLQNVFRIASRNH--PCRNGTVKARGSALLELVPEIKKNLEDFEL : 75  
 PepperB : -----MDTLRTPNNELEF--HGFG--VKVSASFSSVKSQFGAKKFCGLG---SRSVCVKASSSALLELVPEIKKNLEDFEL : 71  
 TomatoB : -----MDTLTKTPNNELEFIPHHGF--AVKASTRSEKIHNFGRKFCETL---GRSVCVKGSSSALLELVPEIKKNLEDFEL : 73  
 TobaccoB : -----MDTLTKTPNKLEFELHPVHGF--VKASSFNSVKPIHFGSRKICENWG---KGVCVKAKSSALLELVPEIKKNLEDFEL : 73  
 MarigoldB : -----MDTLRTYNSFEFVHPSNKFAGNLLNQLNQSKSQFQDFRFGPKSQFGLGQYCVKASSSALLELVPEIKKNLEDFEL : 80  
 DaffodiB : -----MDTLRTHNRLELLYPLHELA--KRHFLLSPSPNPQPNPFKFSRKPQYKCRNGYIGVSSNQLLDLVPEIKKNLEDFEL : 77

PotatoE :  
 ArabidopsisE : IG-----DGAIDHWITGCGPAGLALAAESAKLGLKVLIGPDLIP---FTNNGVMEDEFNDLGLQKQIEHVAROTLVYLDODDPIIGRAYGRVSRHLHEELLKRCVEA : 54  
 AdonisE1 : FG-----ESWDLVWIGCGPAGLSUAAEAAKGLKVLIGPDLIP---FTNNGVMEDEFNDLGLQKQIEHVAROTLVYLDODDPIIGRAYGRVSRHLHEELLKRCVES : 205  
 AdonisE2 : FG-----ESWDLVWIGCGPAGLSUAAEAAKGLKVLIGPDLIP---FTNNGVMEDEFNDLGLQKQIEHVAROTLVYLDODDPIIGRAYGRVSRHLHEELLKRCVES : 204  
 LettuceEE : IG-----NCTLDLWVIGCGPAGLALAAESAKLGLKVLIGPDLIP---FTNNGVMEDEFNDLGLQKQIEHVAROTLVYLDODDPIIGRAYGRVSRHLHEELLKRCVES : 209  
 TomatoE : AG-----QTVLDLWVIGCGPAGLALAAESAKLGLKVLIGPDLIP---FTNNGVMEDEFNDLGLQKQIEHVAROTLVYLDODDPIIGRAYGRVSRHLHEELLKRCVEA : 202  
 MarigoldE : IGGGDSNCTLDLWVIGCGPAGLALAAESAKLGLKVLIGPDLIP---FTNNGVMEDEFNDLGLQKQIEHVAROTLVYLDODDPIIGRAYGRVSRHLHEELLKRCVES : 191  
 ArabidopsisB : PLYDTSKQVVDLAVVGGPAGLAVAQVSEAGLSVCSIDPS-IPKLIMPNNYGVWVDEFEANDLDCDLDITWSSGAVVYDEGVKKDLSRPYGRVNRKQLKSKMLQKQVTN : 181  
 AdonisB : PLYDPSRGIVVDLAVVGGPAGLAVAQVSEAGLSVCSIDPS-IPKLIMPNNYGVWVDEFEANDLDCDLDITWSSGAVVYDEGVKKDLSRPYGRVNRKQLKSKMLQKQVTN : 184  
 PepperB : PLYDPSKGVVDLAVVGGPAGLAVAQVSEAGLSVCSIDPS-IPKLIMPNNYGVWVDEFEANDLDCDLDITWSSGAVVYDEGVKKDLSRPYGRVNRKQLKSKMLQKQVTN : 180  
 TomatoB : PLYDPSKGVVDLAVVGGPAGLAVAQVSEAGLSVCSIDPS-IPKLIMPNNYGVWVDEFEANDLDCDLDITWSSGAVVYDEGVKKDLSRPYGRVNRKQLKSKMLQKQVTN : 182  
 TobaccoB : PLYDPSKGLVVDLAVVGGPAGLAVAQVSEAGLSVCSIDPS-IPKLIMPNNYGVWVDEFEANDLDCDLDITWSSGAVVYDEGVKKDLSRPYGRVNRKQLKSKMLQKQVTN : 182  
 MarigoldB : PLYDPSRNVVDLAVVGGPAGLAVAQVSEAGLSVCSIDPS-IPKLIMPNNYGVWVDEFEANDLDCDLDITWSSGAVVYDEGVKKDLSRPYGRVNRKQLKSKMLQKQVTN : 189  
 DaffodiB : PLYDPSKALITLDLAVVGGPILARSCTSLG--GGLSVSVSIDPS-IPKLIMPNNYGVWVDEFEANDLDCDLDITWSSGAVVYDEGVKKDLSRPYGRVNRKQLKSKMLQKQVTN : 185

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

TDS260" S6EFD260

PotatoE : GVLNLSKQDRIVEATNGHSLVECEGDVITPCRFVTIVASGAAGKFLQVELGGPRVSVQTAIVGEVEVDNNPFDPSLWVFMDYRDY --- VRHDAQSLEAKIPTFLYAMPM : 161  
 ArabidopsisE : GSYLSSKQDSITEASDGLRLVACDDNNVITPCRLATIVASGAAGSKLLOVEVGGPRVSVQTAIVGEVEVENSYPDPDQWVFMDYRDY --- TNEKVSRLAEAKIPTFLYAMPM : 312  
 AdonisE1 : GSYLDSKVERITEAGDGHSLWCENEIFIPCRLATIVASGAAGSKLLEVEVGGPRVSVQTAIVGEVEVENNYPDPNLMVFMDYRDY --- MQQKLQCESEEEYPTFLYAMPM : 311  
 AdonisE2 : GSYLNSKVERITEAGDGHSLWCENEIFIPCRLATIVASGAAGSKLLEVEVGGPRVSVQTAIVGEVEVENNYPDPNLMVFMDYRDY --- MQQKLQCESEEEYPTFLYAMPM : 311  
 LettuceEE : GSYLSSKVERITEAPNGYSLIECEGNITPCRLATIVASGAAGSKFLEVEVGGPRVSVQTAIVGEVEVENNYPDPNLMVFMDYRDY --- SKHKPESLEAKIPTFLYAMPM : 316  
 TomatoE : GVLNLSKQDRIVEATNGHSLVECEGDVITPCRFVTIVASGAAGKFLQVELGGPRVSVQTAIVGEVEVDNNPFDPSLWVFMDYRDY --- LRHDAQSLEAKIPTFLYAMPM : 309  
 MarigoldE : GSYLSSKVERITEAPNGLSLIECEGNITPCRLATIVASGAAGSKLLOVEVGGPRVSVQTAIVGEVEVENNYPDPNLMVFMDYRDY --- TKHKSQSLEAQIPTFLYAMPM : 298  
 ArabidopsisB : GVKFHQSKVITNVH-EEANSTVWCSDGKIQASVLDATG-FSRCLVQYD-KPYNPGYQVAYGIVAEVDGHPFDVDKWFMDRQKHLDSYPELKERNKIPPTFLYAMPF : 288  
 AdonisB : GVKFHQAKVTKVTH-EESKSLLTQNDGTTIQTATVLDATG-FSRCLVQYD-KPYNPGYQVAYGIVAEVEEHFPTDQKLFMDRQSHLNEKLELDKDNKRLPTFLYAMPF : 291  
 PepperB : GVKFHQAKVTKVTH-EESKSLLTQNDGTTIQTATVLDATG-FSRCLVQYD-KPYNPGYQVAYGIVAEVEEHFPTDQKLFMDRQSHLNEKLELDKDNKRLPTFLYAMPF : 287  
 TomatoB : GVKFHQAKVTKVTH-EESKSLLTQNDGTTIQTATVLDATG-FSRCLVQYD-KPYNPGYQVAYGIVAEVEEHFPTDQKLFMDRQSHLNEKLELDKDNKRLPTFLYAMPF : 289  
 TobaccoB : GVKFHQAKVTKVTH-EESKSLLTQNDGTTIQTATVLDATG-FSRCLVQYD-KPYNPGYQVAYGIVAEVEEHFPTDQKLFMDRQSHLNEKLELDKDNKRLPTFLYAMPF : 289  
 MarigoldB : GVKFHQAKVTKVTH-EELKSLLTQNDGTTIQTATVLDATG-FSRCLVQYD-KPYNPGYQVAYGIVAEVEEHFPTDQKLFMDRQSHLNEKLELDKDNKRLPTFLYAMPF : 289  
 DaffodiB : GVRFHQATVVKAMH-EEESKSLLTQNDGTTIQTATVLDATG-FSRCLVQYD-KPYNPGYQVAYGIVAEVEEHFPTDQKLFMDRQSHLNGKAEELNERNKIPPTFLYAMPF : 292

PotatoE : SPTRVFEETCLASKOMPFDLLKKMLRLNTEGVRIKEIVEEESWYIPVGGSLPNTQKTLAFGAASWHPATGYSVRSLEAPKCAFVLANTLRQNHKSNMLTSS : 271  
 ArabidopsisE : TKSRLFEETCLASKOMPFDLLKKMLRLNTEGVRIKEIVEEESWYIPVGGSLPNTQKTLAFGAASWHPATGYSVRSLEAPKCAFVLANTLRQNHKSNMLTSS : 271  
 AdonisE1 : SPTRVFEETCLASKOMPFDLLKKMLRLNTEGVRIKEIVEEESWYIPVGGSLPNTQKTLAFGAASWHPATGYSVRSLEAPKCAFVLANTLRQNHKSNMLTSS : 420  
 AdonisE2 : SPTRVFEETCLASKOMPFDLLKKMLRLNTEGVRIKEIVEEESWYIPVGGSLPNTQKTLAFGAASWHPATGYSVRSLEAPKCAFVLANTLRQNHKSNMLTSS : 421  
 LettuceEE : SPTRVFEETCLASKOMPFDLLKKMLRLNTEGVRIKEIVEEESWYIPVGGSLPNTQKTLAFGAASWHPATGYSVRSLEAPKCAFVLANTLRQNHKSNMLTSS : 421  
 TomatoE : SPTRVFEETCLASKOMPFDLLKKMLRLNTEGVRIKEIVEEESWYIPVGGSLPNTQKTLAFGAASWHPATGYSVRSLEAPKCAFVLANTLRQNHKSNMLTSS : 426  
 MarigoldE : SPTRVFEETCLASKOMPFDLLKKMLRLNTEGVRIKEIVEEESWYIPVGGSLPNTQKTLAFGAASWHPATGYSVRSLEAPKCAFVLANTLRQNHKSNMLTSS : 418  
 ArabidopsisB : SSNRIFLEETSLVARPGLMEDIQERWARLKHGILNKKVKSIEDEHCHVTPVGGSLPVLQORVVGIGGTAGWHPSTGYMVARTLAAAPLVANATVRYLGPSSN-----S : 408  
 AdonisB : SSKIFLEETSLVARPGLMEDIQERWARLKHGILNKKVKSIEDEHCHVTPVGGSLPVLQORVVGIGGTAGWHPSTGYMVARTLAAAPLVANATVRYLGPSSN-----S : 393  
 PepperB : SSNRIFLEETSLVARPGLMEDIQERWARLKHGILNKKVKSIEDEHCHVTPVGGSLPVLQORVVGIGGTAGWHPSTGYMVARTLAAAPLVANATVRYLGPSSN-----S : 395  
 TomatoB : SSNRIFLEETSLVARPGLMEDIQERWARLKHGILNKKVKSIEDEHCHVTPVGGSLPVLQORVVGIGGTAGWHPSTGYMVARTLAAAPLVANATVRYLGPSSN-----S : 391  
 TobaccoB : SSNRIFLEETSLVARPGLMEDIQERWARLKHGILNKKVKSIEDEHCHVTPVGGSLPVLQORVVGIGGTAGWHPSTGYMVARTLAAAPLVANATVRYLGPSSN-----S : 393  
 MarigoldB : SSNRIFLEETSLVARPGLMEDIQERWARLKHGILNKKVKSIEDEHCHVTPVGGSLPVLQORVVGIGGTAGWHPSTGYMVARTLAAAPLVANATVRYLGPSSN-----S : 393  
 DaffodiB : SSNRIFLEETSLVARPGLMEDIQERWARLKHGILNKKVKSIEDEHCHVTPVGGSLPVLQORVVGIGGTAGWHPSTGYMVARTLAAAPLVANATVRYLGPSSN-----S : 403

FIG. 25B



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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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"3560" 502060

## FIG. 25C

	*	460	*	480	*	500	*	520	*	540	*
PotatoE	:	STPS-ISTQAVNTLWQERKQPSFELFGLALILQIDJEGERSFERAFERVPKMAQGFEGSSLSXADJMLFAFYMFIIAPNDMRGLIRHLLSDPTGATLIRTYLTF--	:	378							
ArabidopsisE	:	-----NISRQAMPDLWPPEKQRAFLFGLALIVQEDJEGIPSFERTFERLPKMAQGFEGSTLITSGDLVLFALYMFVISPNNLRKGLINHLISDPTGATMIKTYLKV--	:	524							
AdonisE1	:	SSAVNISQAVSSSLWPKEKQRAFLFGLLEIVQIDJEAIRTFERTFERLPMAAGFEGSSLSFDLVLFSSMYMFVLAPNSMPSLVRHLLSDPSGAMVVRAYLER--	:	529							
AdonisE1	:	SSAVNISQAVSSSLWPKEKQRAFLFGLLEIVQIDJEAIRTFERTFERLPMAAGFEGSSLSFDLVLFSSMYMFVLAPNSMPSLVRHLLSDPSGAMVVKAYLER--	:	529							
LettuceEE	:	KYT-NISQAWETLWPIERKQRAFLFGLSHIVNDJEGTRTFERTFERLPKMAAGFEGSSLSSTDLITFALYMFVIAPHSLPMLVRHLLSDPTGATMKAYLTI--	:	533							
TomatoE	:	SSIPSISTQAVNTLWQERKQPSFELFGLALILQIDJEGIPSFERAFERVPKMAQGFEGSSLSXADJMLFAFYMFIIAPNDMRGLIRHLLSDPTGATLIRTYLTF--	:	526							
MarigoldE	:	RYTTNISQAWETLWPIERKQRAFLFGLALIVQIDJEGTRTFERTFERLPMAAGFEGSSLSSTDLITFALYMFIIAPHSLPMLVRHLLSDPTGATMKAYLTI--	:	516							
ArabidopsisB	:	LRGDQLSAEVMRDLWPIERRRQREFCFQMDILLKLDIDATRRFDFAFEDLQPHYMAIGFESSRFLPELLVFGLSLFSHASNTSRLEIMTK-GTVP-LAKMINNLVQORD	:	501							
AdonisB	:	-SGNELSAEVMKDLWPIERRRQREFCFQMDILLKLDIQGTRRFDAFFDLEPHYMAIGFESSRFLPELLVFGLSLFSHASNTSRLEIMTK-GTVP-LVNMWNLIPDID	:	502							
PepperB	:	-SGDELSAAVMKDLWPIERRRQREFCFQMDILLKLDIPATRRFDFAFEDLEPRYMAIGFESSRFLPELVFGLSLFSHASNTSRLEIMTK-GTVP-LVHMNNLLQOKE	:	498							
TomatoB	:	-SGNELSTAVMKDLWPIERRRQREFCFQMDILLKLDIPATRRFDFAFEDLEPRYMAIGFESSRFLPELVFGLSLFSHASNTSRLEIMTK-GTVP-LVNMNNLLQOKE	:	500							
TobaccoB	:	-LGNELSAVMKDLWPIERRRQREFCFQMDILLKLDIPATRRFDFAFEDLEPRYMAIGFESSRFLPELVFGLSLFSHASNTSRLEIMTK-GTVP-LVNMNNLLQOKE	:	500							
MarigoldB	:	VTGDDLAGIMRELWPIERRRQREFCFQMDILLKLDJEGTRRFDAFFDLEPRYMAIGFESSRFLPELVFGLSLFSGHASNTCRVEIMAK-GTVP-LATMIGNLVQORD	:	511							
DaffodilB	:	-SGNDLSADVMKDLWPIERRRQREFCFQMDILLKLDJEGTRRFDAFFDLEPRYMAIGFESSRFLPELVFGLSLFSGHASNTCKLEIMAK-GTVP-LVNMNNLVQORD	:	503							

## FIG. 26A

	*	20	*	40	*	60	*	80	*	100	*
PotatoE	:	MECVGARNF-AAMAVSTFPSMS-CRRKFPVVKRYSYRNI RFL-CSV--PASGGSSGSESCVAVREDF--ADEEDFYKAGGSEILFVQMQQKMDDETSKLVDKLPPIIS	:	103							
ArabidopsisE	:	MELLGVRNL-----ISSCPVMT-FGTRNLSKSLAYNIHRYGSSCRVDFQVADGGSSRSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPPIP	:	102							
AdonisE1	:	MELLGVRNL-----ISSCPVMT-FGTRNLSKSLAYNIHRYGSSCRVDFQVADGGSSRSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPPIP	:	102							
AdonisE2	:	MECFGARNTATMAVFTCPRTFCNIRHKFSLLKQRRFTNLSA-SSSLRQIKCSAKSDR--CWVQKQISVADEEDYKAGGSELLFVQMQQTKSMEKQAKLADKLPPPIP	:	107							
LettuceEE	:	MECVGVQNV-GAMAVLTPRLN-----RMSGGELCQKSI FLAY-EQY--ESKCNSSGSDSCVVDKEDF--ADEEDYKAGGSQLFVQMQQKMDQSSKLSDEL RQIS	:	100							
TomatoE	:	MSMRAG-IMTATMAAFTCPREFM-----TSIRYT-----LWKQEI--EEEEEDYKAGGSELLFVQMQQKNSMDAQSSLSQKLPRVP	:	84							

	*	120	*	140	*	160	*	180	*	200	*	220
PotatoE	:	IG-----DGALEHVVIGCGPAGLAAEASAKLGLKVGLEIGPOLPTNNYGVWDEENJLGLQKCTEHVWRTIIVYLDODDPIILIGRAYGRVSRHLHEELKRCVFEAGVL	:	57								
ArabidopsisE	:	FG-----ESWMLVVIIGCGPAGLSAAEAANKLGLKVGLEIGPOLPTNNYGVWDEEFKJLGLERCIEHAWKOTIIVYLDNDAPVLIIGRAYGRVSRHLHEELKRCVFEAGVL	:	208								
AdonisE1	:	FG-----ESWMLVVIIGCGPAGLSAAEAANKLGLKVGLEIGPOLPTNNYGVWDEEFKJLGLERCIEHAWKOTIIVYLDNDAPVLIIGRAYGRVSRHLHEELKRCVFEAGVL	:	207								
AdonisE2	:	FG-----ESWMLVVIIGCGPAGLSAAEAANKLGLKVGLEIGPOLPTNNYGVWDEEFKJLGLERCIEHAWKOTIIVYLDNDAPVLIIGRAYGRVSRHLHEELKRCVFEAGVL	:	207								
LettuceEE	:	IG-----NCILDLVVIIGCGPAGLAAEASAKLGLKVGLEIGPOLPTNNYGVWDEEFKJLGLERCIEHAWKOTIIVYLDNDAPVLIIGRAYGRVSRHLHEELKRCVFEAGVL	:	212								
TomatoE	:	AG-----QTVLDLVIIGCGPAGLAAEASAKLGLKVGLEIGPOLPTNNYGVWDEEFKJLGLQKCTEHVWRTIIVYLDODDPIILIGRAYGRVSRHLHEELKRCVFEAGVL	:	205								
MarigoldE	:	IGGGDSNCTIEDLVIIGCGPAGLAAEASAKLGLKVGLEIGPOLPTNNYGVWDEEFKJLGLERCIEHAWKOTIIVYLDNDAPVLIIGRAYGRVSRHLHEELKRCVFEAGVL	:	194								

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 26B

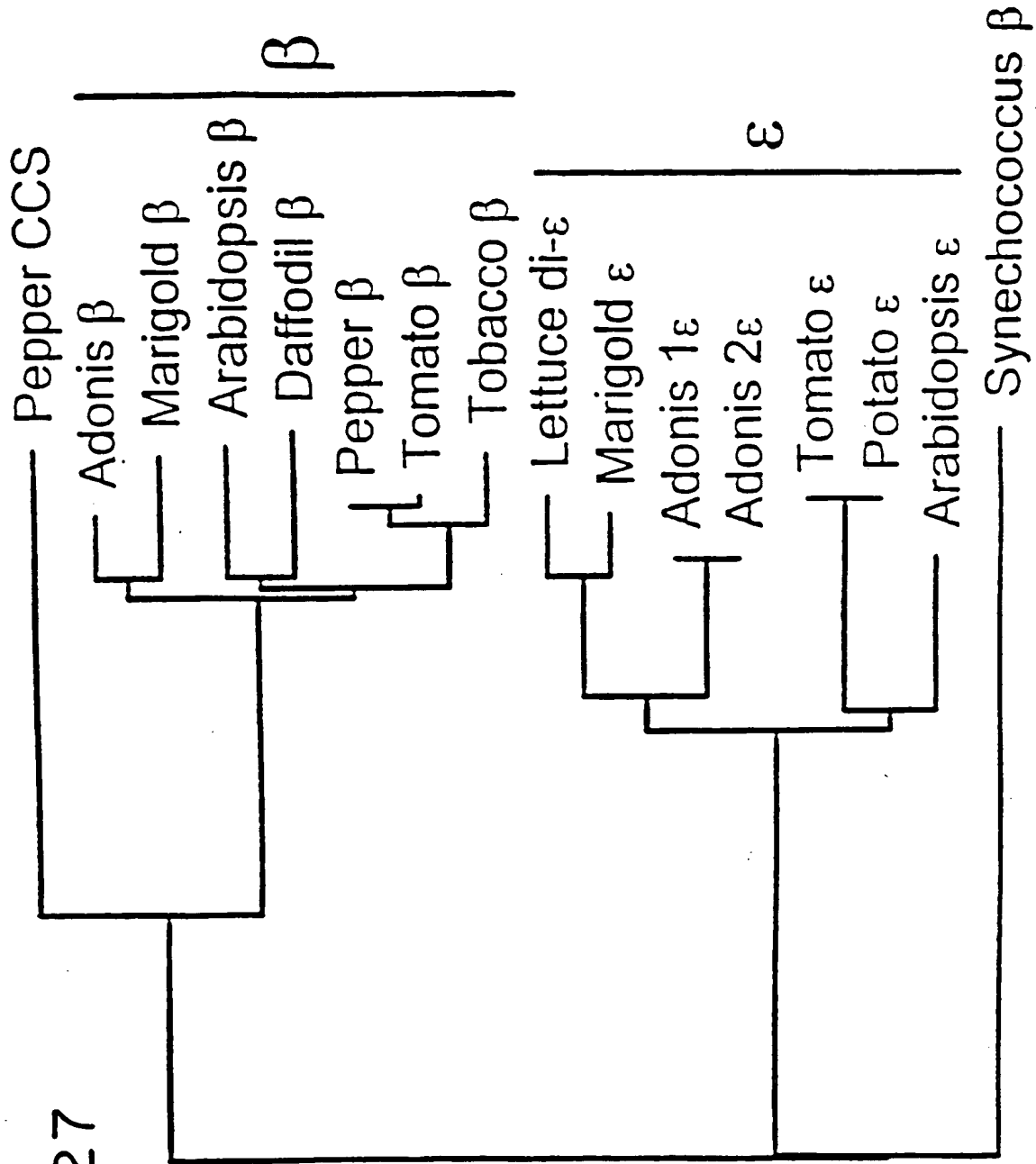
PotatoE	YUNSKVDRIVEATNGHSLVECEGDWV	PCRFVTIVASGAASGKFLQYELGGPRVSVQ	TAYGVEVEVDNNPDPDS	UMVMDYRDYVRHDAQSLEAKYPTFL	YAMPVSPTRVF	167	
ArabidopsisE	YUNSKVDRIVEATNGHSLVECEGDWV	PCRFVTIVASGAASGKFLQYELGGPRVSVQ	TAYGVEVEVDNNPDPDS	UMVMDYRDYVRHDAQSLEAKYPTFL	YAMPVSPTRVF	318	
AdonisE1	YUNSKVDRIVEATNGHSLVECEGDWV	PCRFVTIVASGAASGKFLQYELGGPRVSVQ	TAYGVEVEVDNNPDPDS	UMVMDYRDYVRHDAQSLEAKYPTFL	YAMPVSPTRVF	317	
AdonisE2	YUNSKVDRIVEATNGHSLVECEGDWV	PCRFVTIVASGAASGKFLQYELGGPRVSVQ	TAYGVEVEVDNNPDPDS	UMVMDYRDYVRHDAQSLEAKYPTFL	YAMPVSPTRVF	317	
LettuceEE	YUNSKVDRIVEATNGHSLVECEGDWV	PCRFVTIVASGAASGKFLQYELGGPRVSVQ	TAYGVEVEVDNNPDPDS	UMVMDYRDYVRHDAQSLEAKYPTFL	YAMPVSPTRVF	322	
TomatoE	YUNSKVDRIVEATNGHSLVECEGDWV	PCRFVTIVASGAASGKFLQYELGGPRVSVQ	TAYGVEVEVDNNPDPDS	UMVMDYRDYVRHDAQSLEAKYPTFL	YAMPVSPTRVF	315	
PotatoE	FEETCLASKODAMPFDLLKXKMLRINTL	GVRIKEIYEENSYIPVGGSLPNT	EQKTLAFGAAASMHHPATGYSVVRSL	SEAPKCAFVLANILRQNHKQML	ISSSTPS-I	276	
ArabidopsisE	FEETCLASKODAMPFDLLKXKMLRINTL	GVRIKEIYEENSYIPVGGSLPNT	EQKTLAFGAAASMHHPATGYSVVRSL	SEAPKCAFVLANILRQNHKQML	ISSSTPS-I	422	
AdonisE1	FEETCLASKODAMPFDLLKXKMLRINTL	GVRIKEIYEENSYIPVGGSLPNT	EQKTLAFGAAASMHHPATGYSVVRSL	SEAPKCAFVLANILRQNHKQML	ISSSTPS-I	427	
AdonisE1	FEETCLASKODAMPFDLLKXKMLRINTL	GVRIKEIYEENSYIPVGGSLPNT	EQKTLAFGAAASMHHPATGYSVVRSL	SEAPKCAFVLANILRQNHKQML	ISSSTPS-I	427	
LettuceEE	FEETCLASKODAMPFDLLKXKMLRINTL	GVRIKEIYEENSYIPVGGSLPNT	EQKTLAFGAAASMHHPATGYSVVRSL	SEAPKCAFVLANILRQNHKQML	ISSSTPS-I	431	
TomatoE	FEETCLASKODAMPFDLLKXKMLRINTL	GVRIKEIYEENSYIPVGGSLPNT	EQKTLAFGAAASMHHPATGYSVVRSL	SEAPKCAFVLANILRQNHKQML	ISSSTPS-I	424	
MarigoldE	FEETCLASKODAMPFDLLKXKMLRINTL	GVRIKEIYEENSYIPVGGSLPNT	EQKTLAFGAAASMHHPATGYSVVRSL	SEAPKCAFVLANILRQNHKQML	ISSSTPS-I	414	
PotatoE	STQAWNTLWQERKRORSFFLFGUALI	QVQDIEGIRSF	FRAPFRVPMKQVQGLGSSLSXADLM	IFAFMEI	IAPNDMPRGL	IRHLESDPTGATLIRTYLTF	378
ArabidopsisE	STQAWNTLWQERKRORSFFLFGUALI	QVQDIEGIRSF	FRAPFRVPMKQVQGLGSSLSXADLM	IFAFMEI	IAPNDMPRGL	IRHLESDPTGATLIRTYLTF	524
AdonisE1	STQAWNTLWQERKRORSFFLFGUALI	QVQDIEGIRSF	FRAPFRVPMKQVQGLGSSLSXADLM	IFAFMEI	IAPNDMPRGL	IRHLESDPTGATLIRTYLTF	529
AdonisE2	STQAWNTLWQERKRORSFFLFGUALI	QVQDIEGIRSF	FRAPFRVPMKQVQGLGSSLSXADLM	IFAFMEI	IAPNDMPRGL	IRHLESDPTGATLIRTYLTF	529
LettuceEE	STQAWNTLWQERKRORSFFLFGUALI	QVQDIEGIRSF	FRAPFRVPMKQVQGLGSSLSXADLM	IFAFMEI	IAPNDMPRGL	IRHLESDPTGATLIRTYLTF	533
TomatoE	STQAWNTLWQERKRORSFFLFGUALI	QVQDIEGIRSF	FRAPFRVPMKQVQGLGSSLSXADLM	IFAFMEI	IAPNDMPRGL	IRHLESDPTGATLIRTYLTF	526
MarigoldE	STQAWNTLWQERKRORSFFLFGUALI	QVQDIEGIRSF	FRAPFRVPMKQVQGLGSSLSXADLM	IFAFMEI	IAPNDMPRGL	IRHLESDPTGATLIRTYLTF	516

FIG. 26B

APPROVED	O.G. FIG.		SUBCLASS
BY	CLASS		
DRAFTSMAN			

[illegible]

FIG. 27



## FIG. 28A

GAP of: Arabidopsis epsilon cyclase to Lettuce epsilon cyclase

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	1837	Length:	534
Ratio:	3.499	Gaps:	3

Percent Similarity: 76.381 Percent Identity: 69.905

Match display thresholds for the alignment(s):

| = IDENTITY : = 2 . = 1

Arabidopsis x Lettuce

```

1  MECVGARNF.AAMAVSTFPSW...SCRRKFPVVKRYSYRNIRFGLCSVRA 46
   ||| ||| | ||| | | . . | || ..| . : | :
1  MECFGARNMTATMAVFTCPRFTDCNIRHKFSLLKQRRFTNLSASSSLRQI 50

47  SGGGSSGSESCVAVREDFADEEDFVKAGGSEILFVQMQQNKMDDEQSKLV 96
   | |||||:|||||: ||||. | |: |||
51  KCSAKSDRCVVDKQGISVADEEDYVKAGGSEFFVQMQRTKSMESQSKLS 100

97  DKLPPISIGDGALDHVVIGCGPAGLALAAESA KLGLKVGLIGPDL PFTNN 146
   :|| | ||. || ||||| ||||| ||||| ||||| ||||| |||||
101 EKLAQIPIGNCILDLVVIGCGPAGLALAAESA KLGLNVGLIGPDL PFTNN 150

147 YGVWEDEFNDLGLQKCIHVWRETIVYLD DDKPITIGRAYGRVSRLLHE 196
   ||||:||| |||: ||| |:|: |||| | ||||| ||| |||
151 YGVWQDEFI GLGLEGCIEHSWKDTLVYLD DADPIRIGRAYGRVHRDLLHE 200

197 ELLRRCVESGVSYLSSKVDSITEASDGLRLVACDDNNAIP CRLATVASGA 246
   ||||| |||||: ||| .| |: |: | ||||| |||||
201 ELLRRCVESGVSYLSSKVERITEAPNGYSLIECEGNITIP CRLATVASGA 250

247 ASGKLLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMV FMDYRDTNEKV 296
   |||| |:|: ||||| |||||: ||||. |||| | ||||| :. |
251 ASGKFLEYELGGPRVCVQTAYGIEVEVENNPYD PDL MVFMDYRDFSKHKP 300

297 RSLEAEYPTFLYAMPMTKSRLFFEETCLAS KDVPFDLLKTKLMLRLDTL 346
   ||||. ||||| | |. .: ||||| ||||: |||. |||. ||| || :
301 ESLEAKYPTFLYVMAMSPTKIFFEETCLASREAMPFNLLKSKLMSRLKAM 350

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## FIG. 28B

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347 GIRILKTYEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSL 396
    |||| :|||||||||||||||||||||||||||||||||||||
351 GIRITRTYEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSL 400
    .
397 SEAPKYASVIAEILREETTKQINS.....NISRQAWDTLWPPERKRQRAF 441
    |||| ||.|||.|||::|.:.| |||:||||:|||| |||||
401 SEAPNYAAVIAKILRQDQSKEMISLGKYTNISKQAWETLWPLERKRQRAF 450
    .
442 FLFGLALIVQFDTEGIRSFRTFFRLPKWMWQGLGSTLTSGDLVLFALY 491
    |||||.|| | |||.|||||||||||| |||||.|. | ||::|||
451 FLFGLSHIVLXDLEGTRTFFRTFFRLPKWMWQGLGSSLSTDLIIFALY 500
    .
492 MFVISPNNLRKGLINHLISDPTGATMIKTYLKV* 525
    |||||.||. || |: ||:|||||||:| || :|
501 MFVIAPHSLRMELVRHLLSDPTGATMVKAYLTI* 534

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[illegible]